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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/437,458	11/10/1999	ANTHONY GIORDANO	50093/014001	8009

7590 08/23/2002

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EXAMINER	
LEFFERS JR, GERALD G	

ART UNIT	PAPER NUMBER
1636	23

DATE MAILED: 08/23/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 09/437,458	Applicant(s) GIORDANO ET AL.	
	Examiner Gerry Leffers	Art Unit 1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *04 June 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *3 and 12-34* is/are pending in the application.

4a) Of the above claim(s) *12-27 and 29-31* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *3,28 and 32-34* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☒ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *detailed action/attach* .

DETAILED ACTION

Continued Prosecution Application

The request filed on 1/28/02 for a Continued Prosecution Application (CPA) under 37 CFR 1.53(d) based on parent Application No. 09/437,458 is acceptable and a CPA has been established. An action on the CPA follows.

Election/Restrictions

Applicant's election without traverse of Group 17 (claims 3, 28 and 32-34, drawn towards SEQ ID NO: 170 in Paper No. 22 is acknowledged. Claims 3 and 12-34 are pending in the instant application, with claims 12-27 and 29-31 withdrawn from consideration as drawn towards non-elected inventions.

Oath/Declaration

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because:
Non-initialed and/or non-dated alterations have been made to the oath or declaration. See 37 CFR 1.52(c).

The information for Ashish Xavier has non-initialed alterations to the name.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title.

Claims 3, 28 and 32-34 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific (i.e. specific to the claimed invention) and substantial (i.e. that does not require further experimentation to establish a specific utility) asserted utility or a well established utility.

The rejected claims are directed towards an isolated fusion nucleic acid comprising a first nucleic acid (SEQ ID NO: 17) operably linked to a heterologous second nucleic acid and wherein the mRNA form of the first nucleic acids has RNA binding protein (RBP) binding activity or regulates the functionality of the mRNA form of the fusion nucleic acid. Hybrid transcripts comprising SEQ ID NO: 17 appear to be novel in the art. Therefore, there can be no well established utility for the claimed invention.

Asserted utilities for the claimed chimeric nucleic acids include 1) screening for compounds that affect the RBP binding activity of a particular RNA/RBP binding pair interaction, and/or the mRNA functionality; 2) to identify novel RNA/RBP binding pair interactions; and 3) to modify the expression of a protein encoded by the heterologous nucleic acid portion of the chimeric nucleic acid (e.g. page 10, first paragraph of the instant specification).

SEQ ID NO: 17 is disclosed in the instant specification as being obtained from the human leptin gene (Accession No. NM_000230). The specification generally describes an experiment where a protein extract from cells known to express leptin (3T3-L1) was used to demonstrate binding by an unidentified protein or proteins (RBPs) to an undescribed RNA comprising SEQ ID NO: 17 by either filter binding assay or gel filtration. While poly r(G), heparin and

"unrelated" RNAs were used as non-specific inhibitors in the binding assays, the exact composition of the competing RNAs is not disclosed by the instant specification, making it unclear how specific the observed protein binding actually was for the RNA comprising SEQ ID NO: 17. Also, the actual binding/gel shift data is not provided by the instant specification, making it even harder to determine the specificity of the RBP/RNA interactions in this case. According to the information available at the NCBI web page for Accession No. NM_000230, the sequence represented by SEQ ID NO: 17 is present as a 3' untranslated region in the transcript encoding human leptin.

The asserted utilities are not specific in that the protein or proteins that apparently bound the RNA comprising SEQ ID NO: 17 are not identified in the instant specification. For example, using the claimed nucleic acid hybrid to identify compounds that affect a specific RNA/RBP binding pair cannot be considered to be a specific in the absence of an identified RBP specific to SEQ ID NO: 17. Moreover, the ability of the nucleic acid comprising SEQ ID NO: 17 to modify expression of a protein encoded by the fusion transcript in a specific manner (i.e. stabilize, de-stabilize, sequester, etc.) has not been demonstrated. Therefore, using the chimeric nucleic acid to modify the expression of a protein cannot be considered a specific utility. Finally, use of the claimed chimeric nucleic acid to identify novel RBP/RNA binding pairs cannot be considered specific because it is not known that the proteins that bound the RNA in the binding assay described in the specification do not also bind other RNAs (e.g. RNAs other than the unrelated RNAs used as non-specific inhibitors of binding).

The asserted utilities are not substantial in that for each of the asserted activities, it would require further experimentation in order to confirm a specific utility. For example, it would

require further experimentation to determine the nature and number of different proteins responsible for binding the RNA comprising SEQ ID NO: 17 in the binding assay described in the specification. The asserted utility of using the chimeric nucleic acid to identify its own cognate binding proteins, if any, merely constitutes further experimentation to identify a specific activity.

Claims 3, 28 and 32-34 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 3, 28, 32-34 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The rejected claims are directed towards an isolated fusion nucleic acid comprising a first nucleic acid (SEQ ID NO: 17) operably linked to a heterologous second nucleic acid and wherein the mRNA form of the first nucleic acids has RNA binding protein (RBP) binding

activity or regulates the functionality of the mRNA form of the fusion nucleic acid. Regulating functionality can comprise an alteration in pre-mRNA processing or in the stabilization, translational efficiency, localization, sequestration, editing or splicing functions. Thus, the rejected claims embrace a number of different possible effects of SEQ ID NO: 17 on a chimeric transcript comprising SEQ ID NO: 17.

SEQ ID NO: 17 is disclosed in the instant specification as being obtained from the human leptin gene (Accession No. NM_000230). The specification generally describes an experiment where a protein extract from cells known to express leptin (3T3-L1) was used to demonstrate binding by an unidentified protein or proteins (RBPs) to an undescribed RNA comprising SEQ ID NO: 17 by either filter binding assay or gel filtration. The context of SEQ ID NO: 17 in the total transcript was not described. While poly r(G), heparin and "unrelated" RNAs were used as non-specific inhibitors in the binding assays, the exact composition of the competing RNAs is not described by the instant specification, making it unclear how specific the observed protein binding actually was for the RNA comprising SEQ ID NO: 17. Also, the actual binding/gel shift data is not provided by the instant specification, making it even harder to determine the specificity of the RBP/RNA interactions in this case. There are no relevant working examples or data provided by the instant specification demonstrating the effect the presence of the sequence of SEQ ID NO: 17 on functionality of a transcript comprising SEQ ID NO: 17. No structural/functional basis is provided in the specification for one of skill in the art to envision what are the functional effects, if any, of SEQ ID NO: 17 on a transcript comprising SEQ ID NO: 17.

According to the information available at the NCBI web page for Accession No. NM_000230, the sequence represented by SEQ ID NO: 17 is present as a 3' untranslated region in the transcript encoding human leptin. The prior art does not appear to disclose any embodiment wherein the sequence represented by SEQ ID NO: 17 has been used to modulate the functionality of any RNA, including its own. Therefore, the prior art does not offset the deficiencies of the instant specification as to the actual functional effects of SEQ ID NO: 17 on any transcript comprising the sequence.

Given that the claimed invention comprises a critical element of regulating mRNA functionality that embraces several different processes (e.g. stabilization, translational efficiency, etc.) and given the lack of a structural/functional basis in the instant specification or prior art to envision the actual effect of SEQ ID NO: 17 on a transcript comprising SEQ ID NO: 17, one of skill in the art would not be able to reliably envision the claimed invention. Therefore, one of skill in the art would reasonably conclude that applicants were not in possession of the claimed invention.

Response to Arguments

In response to a similar rejection under 35 U.S.C. 112, first paragraph, for lack of written description, applicants have submitted a declaration under 37 C.F.R. 1.132 from Dr. Anthony Giordano. The declaration by Dr. Giordano clearly teaches that the art recognizes that 5' and 3' UTRs can retain their RBP binding or regulatory activity when linked to heterologous coding sequences. However, the arguments presented by Dr. Giordano are moot as they do not address the current grounds of rejection. In the previous round of rejections, the basis for the rejection was the extremely broad genus of hybrid RNAs encompassed by the claims and the

unpredictability as to whether the claimed UTR sequences would retain their functional activities in the context of a given hybrid transcript. In the current round of rejections, the basis for the rejection is a lack of description of the functional activity (i.e. stabilization, destabilization, translational efficiency, etc.) would be for those embodiments where the claimed UTR (i.e. comprising SEQ ID NO: 17) confers a means of regulating mRNA functionality for the hybrid comprising the claimed UTR. The declaration provided by Dr. Giordano does not address this point.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 3 and 32-34 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 3 and 32-34 are vague and indefinite in that is drawn towards non-elected embodiments (i.e. to SEQ ID NOS other than SEQ ID NO: 17). It would be remedial to amend the claim language to limit the embodiments to SEQ ID NO: 17.

A broad range or limitation together with a narrow range or limitation that falls within the broad range or limitation (in the same claim) is considered indefinite, since the resulting claim does not clearly set forth the metes and bounds of the patent protection desired. Note the explanation given by the Board of Patent Appeals and Interferences in *Ex parte Wu*, 10 USPQ2d 2031, 2033 (Bd. Pat. App. & Inter. 1989), as to where broad language is followed by "such as" and then narrow language. The Board stated that this can render a claim indefinite by

raising a question or doubt as to whether the feature introduced by such language is (a) merely exemplary of the remainder of the claim, and therefore not required, or (b) a required feature of the claims. Note also, for example, the decisions of *Ex parte Steigewald*, 131 USPQ 74 (Bd. App. 1961); *Ex parte Hall*, 83 USPQ 38 (Bd. App. 1948); and *Ex parte Hasche*, 86 USPQ 481 (Bd. App. 1949). In the present instance, claim 33 recites the broad recitation "wherein the nucleic acid is DNA", and the claim also recites "cDNA" which is the narrower statement of the range/limitation. It would be remedial to amend the claims by creating two different dependent claims reciting the limitations of "DNA" or "cDNA".

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gerald G Leffers Jr. whose telephone number is (703) 308-6232. The examiner can normally be reached on 9:30am-6:00pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached on (703) 305-1998. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 305-7939 for regular communications and (703) 305-7939 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

Gerald G Leffers Jr.
Examiner
Art Unit 1636

ggl
August 20, 2002

DAVID GUZO
PRIMARY EXAMINER

09/437,458
Attach Paper #23
File Copy

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Books

Search Nucleotide for Go Clear

Limits Preview/Index History Clipboard Details

Display default Save Text Add to Clipboard

☐1: NM_000230. Homo sapiens lept...[gi:4557714]

MapView, Related Sequences, OMIM, Protein, PubMed, SNP, Taxonomy, UniSTS, LinkOut

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VERSION     NM_000230.1  GI:4557714
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REFERENCE   1  (bases 1 to 3426)
  AUTHORS   Friedman,J.M., Leibel,R.L., Siegel,D.S., Walsh,J. and Bahary,N.
  TITLE     Molecular mapping of the mouse ob mutation
  JOURNAL   Genomics 11 (4), 1054-1062 (1991)
  MEDLINE   92147101
   PUBMED   1686014
REFERENCE   2  (bases 1 to 3426)
  AUTHORS   Zhang,Y., Proenca,R., Maffei,M., Barone,M., Leopold,L. and
            Friedman,J.M.
  TITLE     Positional cloning of the mouse obese gene and its human homologue
  JOURNAL   Nature 372 (6505), 425-432 (1994)
  MEDLINE   95075453
   PUBMED   7984236
REFERENCE   3  (bases 1 to 3426)
  AUTHORS   Masuzaki H, Ogawa Y, Isse N, Satoh N, Okazaki T, Shigemoto M, Mori
            K, Tamura N, Hosoda K, Yoshimasa Y et al.
  TITLE     Human obese gene expression. Adipocyte-specific expression and
            regional differences in the adipose tissue
  JOURNAL   Diabetes 44 (7), 855-858 (1995)
  MEDLINE   95309556
   PUBMED   7789654
REFERENCE   4  (bases 1 to 3426)
  AUTHORS   Green,E.D., Maffei,M., Braden,V.V., Proenca,R., DeSilva,U.,
            Zhang,Y., Chua,S.C. Jr., Leibel,R.L., Weissenbach,J. and
            Friedman,J.M.
  TITLE     The human obese (OB) gene: RNA expression pattern and mapping on
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  JOURNAL   Genome Res. 5 (1), 5-12 (1995)
  MEDLINE   96352898
   PUBMED   8717050
REFERENCE   5  (bases 1 to 3426)
  AUTHORS   Isse N, Ogawa Y, Tamura N, Masuzaki H, Mori K, Okazaki T, Satoh N,
            Shigemoto M, Yoshimasa Y, Nishi S et al.
  TITLE     Structural organization and chromosomal assignment of the human
            obese gene
  JOURNAL   J. Biol. Chem. 270 (46), 27728-27733 (1995)
  MEDLINE   96070903
   PUBMED   7499240
REFERENCE   6  (bases 1 to 3426)
  AUTHORS   Gong,D.W., Bi,S., Pratley,R.E. and Weintraub,B.D.
  TITLE     Genomic structure and promoter analysis of the human obese gene
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JOURNAL J. Biol. Chem. 271 (8), 3971-3974 (1996)
MEDLINE 96223958
PUBMED 8626726
REFERENCE 7 (bases 1 to 3426)
AUTHORS Niki T, Mori H, Tamori Y, Kishimoto-Hashirmoto M, Ueno H, Araki S, Masugi J, Sawant N, Majithia HR, Rais N et al.
TITLE Human obese gene: molecular screening in Japanese and Asian Indian NIDDM patients associated with obesity
JOURNAL Diabetes 45 (5), 675-678 (1996)
MEDLINE 96198511
PUBMED 8621021
REFERENCE 8 (bases 1 to 3426)
AUTHORS Comuzzie,A.G., Hixson,J.E., Almasy,L., Mitchell,B.D., Mahaney,M.C., Dyer,T.D., Stern,M.P., MacCluer,J.W. and Blangero,J.
TITLE A major quantitative trait locus determining serum leptin levels and fat mass is located on human chromosome 2
JOURNAL Nat. Genet. 15 (3), 273-276 (1997)
MEDLINE 97207647
PUBMED 9054940
REFERENCE 9 (bases 1 to 3426)
AUTHORS Clement,K., Vaisse,C., Lahlou,N., Cabrol,S., Pelloux,V., Cassuto,D., Gourmelen,M., Dina,C., Chambaz,J., Lacorte,J.M., Basdevant,A., Bougneres,P., Lebouc,Y., Froguel,P. and Guy-Grand,B.
TITLE A mutation in the human leptin receptor gene causes obesity and pituitary dysfunction
JOURNAL Nature 392 (6674), 398-401 (1998)
MEDLINE 98196670
PUBMED 9537324
REFERENCE 10 (bases 1 to 3426)
AUTHORS Friedman,J.M. and Halaas,J.L.
TITLE Leptin and the regulation of body weight in mammals
JOURNAL Nature 395 (6704), 763-770 (1998)
MEDLINE 99010835
PUBMED 9796811
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from U43653.1.
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     2641 gagcgctttc tggaaaagag gagtttcgag gtagagtttg aaggaggtga gggatgtgaa
     2701 ttgcctgcag agagaagcct gttttgttgg aaggtttggt gtgtggagat gcagaggtaa
     2761 aagtgtgagc agtgagttac agcgagaggc agagaaagaa gagacaggag ggcaagggcc
     2821 atgctgaagg gaccttgaag ggtaaagaag tttgatatta aaggagttaa gagtagcaag
     2881 ttctagagaa gaggctggtg ctgtggccag ggtgagagct gctctggaaa atgtgaccca
```

```
     2941 gatcctcaca accacctaat caggctgagg tgtcttaagc cttttgctca caaaacctgg
     3001 cacaatggct aattcccaga gtgtgaaact tcctaagtat aaatggttgt ctgtttttgt
     3061 aacttaaaaa aaaaaaaaaa agtttggccg ggtgcggtgg ctcacgcctg taatcccagc
     3121 actttgggag gccaaggtgg ggggatcaca aggtcactag atggcgagca tcctggccaa
     3181 catggtgaaa ccccgtctct actaaaaaca caaaagttag ctgagcgtgg tggcgggcgc
     3241 ctgtagtccc agccactcgg gaggctgaga caggagaatc gcttaaacct gggaggcgga
     3301 gagtacagtg agccaagatc gcgccactgc actccggcct gatgacagag cgagattccg
     3361 tcttaaaaaa aaaaaaaaaa aaagtttgtt tttaaaaaaa tctaaataaa ataactttgc
     3421 cccctg
//
```

Revised: July 5, 2002.

Attach #23

L Number	Hits	Search Text	DB	Time stamp
1	857	giordano-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 19:57
7	268	xavier-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 19:57
13	3	giordano-$.in. and xavier-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 19:58
19	2	6273893.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 19:58
25	1122	giordano-$.in. or xavier-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 19:59
31	7	(giordano-$.in. or xavier-$.in.) and utr	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:00
37	1	(giordano-$.in. or xavier-$.in.) and leptin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:01
43	206	leptin with (gene or rna or message or transcript or cdna)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:02
49	10	(leptin with (gene or rna or message or transcript or cdna)) with (fusion or chimer$4 or hybrid)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/19 20:03

US-PAT-NO: 6258559

DOCUMENT-IDENTIFIER: US 6258559 B1

TITLE: Method for producing proteins in transformed Pichia

---------- KWIC ----------

In the following examples, Pichia methanolica strain PMAD16 was used as a host strain. This strain is derived from type strain CBS 6515 and is described by Raymond et al., Yeast 14:11 (1998), and by Raymond, "Recombinant Protein Expression in Pichia methanolica," in Gene Expression Systems: Using Nature for the Art of Expression, Fernandez and Hoeffler (eds.), pages 193-209 (Academic Press, Inc. 1999). The host strain carries both alcohol utilization genes AUG1 and AUG2 and is deleted for PEP4 and PRB1 proteases. For these studies, the Pichia contained an expression vector derived from pCZR1 34, which comprises an AUG1 promoter, AUG1 terminator, and ADE2 as a selectable marker (Raymond et al., Yeast 14:11 (1998)). A chimeric gene comprising the following elements was inserted between the AUG1 promoter and terminator: a S. cerevisiae a-factor prepro sequence, a Glu:Glu tag or a FLAG tag, and a human leptin gene. The human leptin gene has been described by Zhang et al., Nature 372:425 (1994). An illustrative method for constructing a plasmid that comprises a human leptin gene is described by Raymond et al., BioTechniques 26:134 (1999), and an exemplary human leptin amino acid sequence is provided by SEQ ID NO:7 (GenBank accession No. 4139908).

(FILE 'HOME' ENTERED AT 20:06:59 ON 19 AUG 2002)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 20:07:08 ON 19 AUG 2002

L1 13478 S (GIORDANO, ?)/IN,AU
L2 2724 S (XAVIER, ?)/IN,AU
L3 6 S L1 AND L2
L4 16196 S L1 OR L2
L5 16 S L4 AND LEPTIN
L6 0 S L4 AND (LEPTIN (S) UTR)
L7 3 S L4 AND (LEPTIN (S) (GENE OR RNA OR TRANSCRIPT OR MRNA))
L8 1 DUPLICATE REMOVE L7 (2 DUPLICATES REMOVED)
L9 13 S L5 NOT L7
L10 5 DUPLICATE REMOVE L9 (8 DUPLICATES REMOVED)
L11 50 S (FUSION OR CHIMER? OR HYBRID) (S) (LEPTIN (S) (GENE OR RNA
OR
L12 3 S L11 (S) REPORTER
L13 1 DUPLICATE REMOVE L12 (2 DUPLICATES REMOVED)
L14 25 DUPLICATE REMOVE L11 (25 DUPLICATES REMOVED)
L15 17531 S (GONG, ?)/IN,AU
L16 22 S L15 AND LEPTIN
L17 11 S L16 AND (LEPTIN (S) (GENE OR RNA OR TRANSCRIPT OR MRNA))
L18 3 DUPLICATE REMOVE L17 (8 DUPLICATES REMOVED)

#23

STIC-Biotech/ChemLib 686449

From: Fredman, Jeffrey
Sent: Wednesday, June 12, 2002 3:00 PM
To: STIC-Biotech/ChemLib
Cc: Leffers, Gerald
Subject: FW: 09/437,458

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----
From: Leffers, Gerald
Sent: Wednesday, June 12, 2002 2:56 PM
To: Fredman, Jeffrey
Subject: 09/437,458

11A09
1636
11E12

Hi Jeff, please approve a RUSH search/interference search for this application for SEQ ID NO: 17 (~239 nucleotides).
Thanks, Gerry Leffers

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpm** and **.rnpn**
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.

Searcher: D. Schreiber
Phone: 308-4292
Location: CM1 6A03
Date Picked Up: 6/13
Date Completed: 6/14
Searcher Prep/Review: ____
Clerical: ____
Online time: 5

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: ____
Structures: ____
Bibliographic: ____
Litigation: ____
Full text: ____
Patent Family: ____
Other: ____

VENDOR/COST(where applic.)
STN: ____
DIALOG: ____
Questel/Orbit: ____
DRLink: ____
Lexis/Nexis: ____
Sequence Sys.: ____
WWW/Internet: ____
Other (specify): Compugen

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 13, 2002, 12:49:48 ; Search time 266.48 Seconds
(without alignments)
1539.862 Million cell updates/sec

Title: US-09-437-458-17
Perfect score: 239
Sequence: 1 ctggtttcatttctactgtg.....gtgagatcattttcttatct 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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5: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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10: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
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15: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
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19: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	239	100.0	239	22	AAH27148	Human leptin gene
2	239	100.0	3408	22	AAD17487	Human leptin (LEP)
3	239	100.0	3426	20	AAX59851	SEQ ID 4 of WO9925
4	239	100.0	4258	23	AAS78055	DNA encoding novel
5	80.6	33.7	2793	17	AAT16372	Obesity protein co
6	80.6	33.7	2793	21	AAC62565	Murine OB cDNA. M
7	80.6	33.7	2793	21	AAC62645	Murine OB cDNA. M
8	80.6	33.7	2793	21	AAA12287	Murine OB DNA. Mu
9	80.6	33.7	2793	22	AAF76943	Murine leptin cDNA
10	73.4	30.7	5917	19	AAV17090	Porcine adipocyte
11	36	15.1	12237	24	ABL34358	Human immune syste
12	35.8	15.0	5314	24	ABL32161	Human immune syste
13	34.4	14.4	14861	24	ABL33195	Human immune syste
14	34.4	14.4	14861	24	AAS61203	Human gene regulat
15	34.2	14.3	311	8	AAN70097	Sequence of Ex pro
16	34.2	14.3	311	9	AAN81303	Ex-promoter. Baci
17	34.2	14.3	311	11	AAQ05183	Ex promoter derive
18	34.2	14.3	5551	24	AAS61099	Human gene regulat
19	33.6	14.1	5449	24	ABL33640	Human immune syste
20	33.6	14.1	13573	24	ABL33868	Human immune syste
c 21	33.4	14.0	4116	20	AAX86690	DNA encoding a TAF
22	33	13.8	8420	22	AAS46658	Tumour suppressor
23	32.8	13.7	6392	24	ABL32685	Human immune syste
24	32.8	13.7	6392	24	ABL34507	Human metastasis a
25	32.8	13.7	7119	24	ABL32293	Human immune syste
26	32.6	13.6	16750	22	AAS46313	Tumour suppressor
27	32.6	13.6	16750	24	ABL32520	Human immune syste
28	32.2	13.5	5179	24	ABL33997	Human immune syste
29	32.2	13.5	6040	24	ABL32066	Human immune syste
30	31.8	13.3	440	22	AAH94193	Human foetal cDNA,
31	31.8	13.3	440	22	AAH94554	Human foetal cDNA,
32	31.8	13.3	5430	22	AAS46292	Tumour suppressor
33	31.8	13.3	13125	24	ABL33227	Human immune syste
34	31.8	13.3	13125	24	ABL34557	Human metastasis a
c 35	31.6	13.2	665	22	ABA06667	Human cDNA SEQ ID
c 36	31.6	13.2	665	22	AAS28864	Human immunoglobul
37	31.6	13.2	73334	24	ABL34125	Human immune syste
38	31.4	13.1	6398	23	ABL12502	Drosophila melanog
39	31.4	13.1	7384	24	ABL32747	Human immune syste
40	31.4	13.1	15592	22	AAS46453	Tumour suppressor
41	31.4	13.1	15592	24	ABL33326	Human immune syste
42	31.4	13.1	15767	24	ABL33206	Human immune syste
43	31.4	13.1	15767	24	ABL34552	Human metastasis a
44	31.2	13.1	6229	24	ABL32265	Human immune syste
45	31.2	13.1	6568	24	ABL32447	Human immune syste

ALIGNMENTS

RESULT 1
AAH27148
ID AAH27148 standard; DNA; 239 BP.
XX
AC AAH27148;
XX
DT 08-AUG-2001 (first entry)
XX
DE Human leptin gene UTR region with RBP binding ability.
XX
KW Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;
KW stroke; cardiovascular disease; hypertension; cancer; inflammation; ds;
KW leptin; metabolic disorder; obesity; diabetes.
XX
OS Homo sapiens.
XX
PN WO200134624-A1.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30888.
XX
PR 10-NOV-1999; 99US-0437458.
XX
PA (MESS-) MESSAGE PHARM INC.
XX
PI Giordano A, Xavier AK;
XX
DR WPI; 2001-335904/35.
XX
PT New nucleic acids that bind RNA-binding proteins or regulate mRNA
PT function, useful for therapeutic gene regulation, such as in cases of

```
PT   neurodegeneration -
XX
PS   Claim 1; Page 30; 33pp; English.
XX
CC   Sequences AAH27132 - AAH27151 represent human gene untranslated regions
CC   where the corresponding mRNA fragment has RNA binding protein (RBP)
CC   binding activity. RBPs mediate the processing of pre-mRNA, the transport
CC   of mRNA from the nucleus to the cytoplasm, mRNA stabilisation,
CC   translational efficiency, and the sequestration of some mRNAs. Therefore
CC   modification of post-transcriptional protein expression in eukaryotic
CC   cells may be carried out through the targeting specific interactions of
CC   proteins that bind to RBPs. The gene fragments of the invention are used
CC   to identify their optimized sub-fragments, compounds that affect RNA/RBP
CC   interaction or mRNA functionality; or RBPs that interact with the
CC   compounds. Compounds identified using the gene fragments are potentially
CC   useful for therapeutic regulation of gene expression, such as in cases of
CC   neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
CC   inflammation; metabolic disorders (obesity and diabetes) and bacterial or
CC   viral infection. The present sequence is one of gene fragments of the
CC   invention, isolated from the human leptin gene.
XX
     Sequence 239 BP; 54 A; 32 C; 68 G; 85 T; 0 other;


  Query Match             100.0%;  Score 239;  DB 22;  Length 239;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-66;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60

Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239


RESULT   2
AAD17487
ID   AAD17487 standard; cDNA; 3408 BP.
XX
AC   AAD17487;

DT   10-DEC-2001  (first entry)
XX
DE   Human leptin (LEP) cDNA.
XX
KW   Mucosal cell; cell therapy; gene therapy; hyperglycaemia; wound healing;
KW   haemophilia; eye damage; diabetes; obesity; degenerative disorder; ulcer;
KW   beta-cell destruction; kidney tubule calcification; liver degeneration;
KW   diabetic retinopathy; cancer; coronary heart disease; growth disorder;
KW   dyslipidaemia; coagulation disorder; stroke; peripheral vascular disease;
KW   hypertension; wasting syndrome; passive immunisation; immunosuppressive;
KW   Helicobacter pylori; arthritis; cardiovascular disease; ophthalmological;
KW   hypoglycaemic; anorectic; coagulant; cerebroprotective; antimicrobial;
KW   leptin; LEP; vulnerary; cytostatic; hypotensive; cardiant; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             40..543
FT                   /*tag= a
FT                   /product= "Human leptin"
XX
PN   WO200168828-A2.
XX
PD   20-SEP-2001.
XX
PF   12-MAR-2001; 2001WO-IB00722.
XX
PR   13-MAR-2000; 2000US-0188796.
PR   08-DEC-2000; 2000US-0254464.
XX
PA   (ENGE-) ENGENE INC.
XX
PI   Kieffer TJ,  Cheung AT;
XX
DR   WPI; 2001-582445/65.
DR   P-PSDB; AAE10338.
XX
PT   Novel isolated or cultured mucosal cell producing nutrient-regulatable
PT   protein expressed by transgene comprising expression control element
PT   linked with nucleic acid encoding protein, is useful for treating
PT   diabetes -
XX
PS   Disclosure; Fig 17-18; 75pp; English.
XX
CC   The present invention relates to an isolated or cultured mucosal cell
CC   that produces a protein regulatable by a nutrient, where expression of
CC   the protein is conferred by a transgene comprising an expression control
CC   element in operable linkage with a nucleic acid encoding the protein.
CC   The invention is used in cell therapy and gene therapy. Isolated or
CC   cultured mucosal cell is useful for treating a hyperglycaemic condition
CC   such as type I diabetes (insulin-dependent diabetes), where the subject
CC   has a fasting plasma glucose level of greater than 110 mg/dl. It is also
CC   useful for treating obesity or undesirable body mass. Preferably, in
CC   these conditions the mucosal cell expresses insulin, leptin, glucagon-
CC   like peptide (GLP)-1, GLP-2, cholecystokinin (CCK), a glucagon
CC   antagonist, a growth hormone, a clotting factor or an antibody. The
CC   mucosal cells are implanted into a mucosal tissue or non-mucosal tissue
CC   such as liver, pancreas or muscle. Mice strains that develop or are
CC   susceptible to developing a particular disease (e.g. diabetes, cancer,
CC   degenerative disorders etc.) are also useful for introducing therapeutic
CC   proteins in order to study the effect of therapeutic protein expression
CC   in the disease susceptible mouse. Mucosal cell is also useful for
CC   treating insulin-independent (type 2) diabetes, degeneration of pancreas
CC   (beta-cell destruction), kidney tubule calcification, degeneration of
CC   liver, eye damage (diabetic retinopathy), diabetic foot, ulcerations in
CC   mucosa such as mouth and gums, excess bleeding, wound healing or delayed
CC   blood coagulation and increased risk of coronary heart disease, stroke,
CC   peripheral vascular disease, dyslipidaemia, hypertension and obesity.
CC   Mucosal cell also produces protein such as clotting factors to treat
CC   haemophilia and other coagulation disorders, growth factors to treat
CC   growth disorders or wasting syndrome, and antibodies to provide passive
CC   immunisation or protection of a subject against foreign antigens or
CC   pathogens e.g. Helicobacter pylori or to provide treatment of cancer,
CC   arthritis, or cardiovascular disease. The present sequence is human
CC   leptin (LEP) cDNA.
XX
SQ   Sequence 3408 BP; 880 A; 795 C; 911 G; 822 T; 0 other;


  Query Match             100.0%;  Score 239;  DB 22;  Length 3408;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-65;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
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Db    1305 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 1364

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
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Db    1365 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 1424
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Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
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RESULT   3
AAX59851
ID   AAX59851 standard; DNA; 3426 BP.
XX
AC   AAX59851;
XX
DT   28-JUL-1999  (first entry)
XX
DE   SEQ ID 4 of WO9925824.
XX
KW   Mutation; human leptin; marker; obesity; hypogonadism;
KW   leptin secretion; leptin activity; ss.
XX
     Homo sapiens.
XX
PN   WO9925824-A1.
XX
PD   27-MAY-1999.
XX
PF   13-NOV-1998;   98WO-FR02420.
XX
PR   14-NOV-1997;   97FR-0014295.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Camoin L,  Issad T,  Ozata M,  Strobel A,  Strosberg AD;
XX
DR   WPI; 1999-338005/28.
XX
PT   Nucleic acid encoding a non-secreted human leptin mutant
XX
PS   Disclosure; Page 21-23; 31pp; French.
XX
CC   The specification describes a mutated human leptin that has Trp at
CC   position 105. The Arg105Trp mutation is a marker for subjects at risk
CC   of becoming obese, and for suitability of obese subjects for treatment
CC   with leptin. Subjects homozygous for the mutation are severely obese
CC   with hypogonadism, and have exceptionally low levels of leptin in the
CC   serum (the mutant is not secreted); heterozygotes are normal but
CC   carriers. Cells containing the mutated leptin cDNA sequence are used
CC   as model systems for studying mechanism of leptin secretion and
CC   activity, e.g. to differentiate between the reproductive and metabolic
CC   actions of leptin and to identify agents that affect specifically
CC   just one of these actions.
XX
SQ   Sequence 3426 BP; 887 A; 798 C; 920 G; 821 T; 0 other;


  Query Match           100.0%;  Score 239;  DB 20;  Length 3426;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-65;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    1262 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 1321

Qy      61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1322 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 1381

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1382 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 1441

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1442 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 1500


RESULT   4
AAS78055
ID   AAS78055 standard; cDNA; 4258 BP.
XX
AC   AAS78055;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #13859.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG13868.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 13859; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 4258 BP; 1109 A; 993 C; 1174 G; 982 T; 0 other;


  Query Match           100.0%;  Score 239;  DB 23;  Length 4258;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-65;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1278 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 1337

Qy      61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
```

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 1397

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 1457

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcatttttcttatct 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcatttttcttatct 1516


RESULT   5
AAT16372
ID   AAT16372 standard; cDNA; 2793 BP.
XX
AC   AAT16372;
XX
DT   11-SEP-1996  (first entry)
XX
DE   Obesity protein coding sequence.

KW   Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW   food intake; energy expenditure; high blood pressure; cholesterol; human;
KW   gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             57..560
FT                   /*tag= a
FT                   /product= obesity protein
FT   sig_peptide     57..119
FT                   /*tag= b
FT   mat_peptide     120..557
FT                   /*tag= c
XX
PN   GB2292382-A.
XX
PD   21-FEB-1996.
XX
PF   17-AUG-1995;   95GB-0016947.
XX
PR   07-JUN-1995;   95US-0483211.
PR   17-AUG-1994;   94US-0292345.
PR   30-NOV-1994;   94US-0347563.
PR   10-MAY-1995;   95US-0438431.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.

PI   Burley SK,  Friedman JM,  Gajiwala K,  Halaas JL,  Maffei M;
PI   Proenca R,  Zhang Y;
XX
DR   WPI; 1996-099009/11.
DR   P-PSDB; AAR92719.
XX
PT   Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
PT   reducing wt. in treatment of diabetes, high blood pressure and high
PT   cholesterol and for cosmetic reasons
XX
PS   Claim 26; Page 167-169; 304pp; English.
XX
CC   This sequence represents the coding sequence for the mouse obesity
CC   polypeptide (OBP).  OBP (also known as leptin) is a hormone involved in
CC   the regulation of body weight.  The encoded sequence has effects on both
CC   food intake and energy expenditure.  OBP and its analogues are useful for
CC   modifying body weight (optionally combined with known medicaments), for
CC   treating diabetes, high blood pressure or high cholesterol.  This
CC   sequence (and sequences complimentary to it) can be used in gene therapy
CC   for modifying body weight.  The encoded protein can be used for reducing
CC   weight for health or cosmetic reasons in obese humans, or to produce
CC   leaner food animals.  Antagonists of OBP (including antibodies) are
CC   useful for increasing body weight, e.g. for treating weight loss
CC   associated with cancer, or for cosmetic reasons in humans, or for
CC   production of Kobe beef or Foie gras in domestic animals.  OBP antibodies
CC   (Ab) can also be used in diagnostic immunoassays for the presence of OBP.
CC   The formation of Ab-OBP complexes enables in vitro evaluation of levels
CC   of OBP in a sample, especially to detect diseases associated with
CC   elevated or decreased levels, and to monitor treatment of these diseases.
XX
SQ   Sequence 2793 BP; 689 A; 653 C; 740 G; 711 T; 0 other;


  Query Match             33.7%;  Score 80.6;  DB 17;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 1.9e-15;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
          |||||||  ||||||  |||||||||   ||    |    |||||||  ||  |||||
Db   1225 ctggttttgtttctattgtgactgactctatccaaacacgtttgcagcggcattgcc--- 1281

Qy     61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
             ||| |       |     ||||   ||  ||||   ||||||||||||| |||||||
Db   1282 --gggagcataggctaggttattatcaaaagcagatgaattttgtcaagtgtaatatgta 1339

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
           | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 tctatgtgcacctgagggtagaggatgtgttagagggagggtgaaggatccggaa-gtgt 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 tctctgaattacatatgtgtggtaggcttttctgaaagggtgaggcatttt 1449


RESULT   6
AAC62565
ID   AAC62565 standard; cDNA; 2793 BP.
XX
AC   AAC62565;
XX
DT   01-FEB-2001  (first entry)
XX
DE   Murine OB cDNA.
XX
KW   Human; mouse; OB gene; obesity; adiposity; body weight; ss.
XX
OS   Mus sp.
XX
PN   US6124448-A.
XX
PD   26-SEP-2000.
XX
PF   07-JUN-1995;   95US-0488208.
XX
PR   17-AUG-1994;   94US-0292345.
PR   30-NOV-1994;   94US-0347563.
PR   10-MAY-1995;   95US-0438431.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Maffei M,  Proenca R,  Zhang Y,  Friedman JM;
XX
DR   WPI; 2000-601556/57.
DR   P-PSDB; AAB28447.
XX
PT   Nucleic acid primers and probes useful for detecting mutations in
PT   mammalian OB gene associated with regulation of body weight and
PT   adiposity -
XX
PS   Claim 1; Fig 1; 153pp; English.
XX
CC   The present sequence was used in an invention relating to the control of
CC   body weight of animals including humans. Nucleic acids of at
CC   least 10 nucleotides which are hybridisable to a non-coding region of an
CC   OB nucleic acid have been created. The OB gene plays a critical role in
CC   the regulation of body weight and adiposity. The nucleic acids may
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CC   be used as probes or as primers for PCR. They are useful for evaluating
CC   the presence of mutations in the human OB gene or for evaluating the
CC   level of expression of OB mRNA. Defects associated with OB gene
CC   expression result in obese phenotypes.
XX
SQ   Sequence 2793 BP; 689 A; 653 C; 740 G; 711 T; 0 other;


  Query Match             33.7%;  Score 80.6;  DB 21;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 1.9e-15;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           |||||||  ||||||  |||||||||    ||    |    |||||||  ||  |||||
Db    1225 ctggttttgtttctattgtgactgactctatccaaacacgtttgcagcggcattgcc--- 1281

Qy      61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
             ||| |       |     ||||   ||  ||||   |||||||||||||| |||||||
Db    1282 --gggagcataggctaggttattatcaaaagcagatgaattttgtcaagtgtaatatgta 1339

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
             | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db    1340 tctatgtgcacctgagggtagaggatgtgttagagggagggtgaaggatccggaa-gtgt 1398

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
           | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db    1399 tctctgaattacatatgtgtggtaggcttttctgaaagggtgaggcatttt 1449


RESULT   7
AAC62645
ID   AAC62645 standard; cDNA; 2793 BP.
XX
AC   AAC62645;
XX
DT   01-FEB-2001  (first entry)
XX
DE   Murine OB cDNA.
XX
KW   Human; mouse; anabolic; cytostatic; immunostimulant;
KW   OB polypeptide inhibitor; body weight; obesity; OB gene; cancer; AIDS;
KW   anorexia nervosa; hypertension; heart disease; Type II diabetes; ss.
XX
OS   Mus sp.
XX
PN   US6124439-A.

     26-SEP-2000.
XX
PF   07-JUN-1995;   95US-0488214.
XX
PR   17-AUG-1994;   94US-0292345.
PR   30-NOV-1994;   94US-0347563.
PR   10-MAY-1995;   95US-0438431.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Proenca R,  Zhang Y,  Friedman JM;
XX
DR   WPI; 2000-611018/58.
DR   P-PSDB; AAB28466.
XX
PT   Novel antibody to mammalian obesity polypeptide useful for diagnosis
PT   and treatment of weight loss associated with disorders such as cancer,
PT   AIDS and anorexia nervosa -
XX
PS   Disclosure; Fig 1; 150pp; English.
XX
CC   The present sequence was used in an invention relating to the control of
CC   body weight of animals including humans. Antibodies against the mammalian
CC   obesity (OB) polypeptide have been identified. The antibodies are useful
CC   for modulating the activity of OB to control body weight and fat content
CC   and/or to treat certain pathological conditions in which there is
CC   abnormal depression or elevation of body weight. The antibodies are used
CC   to treat weight loss associated with cancer, AIDS and anorexia nervosa.
CC   They are useful for the diagnosis of nutritional disorders such as
CC   obesity and diseases associated with obesity, such as hypertension,
CC   heart disease and Type II diabetes. The kits are used to determine the
CC   presence or amount of OB in the blood or plasma of an individual.
XX
SQ   Sequence 2793 BP; 689 A; 653 C; 740 G; 711 T; 0 other;


  Query Match             33.7%;  Score 80.6;  DB 21;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 1.9e-15;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           |||||||  ||||||  |||||||||    ||    |    |||||||  ||  |||||
Db    1225 ctggttttgtttctattgtgactgactctatccaaacacgtttgcagcggcattgcc--- 1281

Qy      61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
             ||| |       |     ||||   ||  ||||   |||||||||||||| |||||||
Db    1282 --gggagcataggctaggttattatcaaaagcagatgaattttgtcaagtgtaatatgta 1339

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
             | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db    1340 tctatgtgcacctgagggtagaggatgtgttagagggagggtgaaggatccggaa-gtgt 1398

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
           | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db    1399 tctctgaattacatatgtgtggtaggcttttctgaaagggtgaggcatttt 1449


RESULT   8
AAA12287
ID   AAA12287 standard; DNA; 2793 BP.
XX
AC   AAA12287;
XX
DT   18-AUG-2000  (first entry)
XX
DE   Murine OB DNA.
XX
KW   OB gene; body weight; obesity; anorectic; adipose tissue; brain;
KW   murine; ds.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             57..560
FT                   /*tag=  a
FT                   /product= "OB protein"
XX
PN   US6048837-A.
XX
PD   11-APR-2000.
XX
PF   07-JUN-1995;   95US-0485942.
XX
PR   17-AUG-1994;   94US-0292345.
PR   30-NOV-1994;   94US-0347563.
PR   10-MAY-1995;   95US-0438431.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Proenca R,  Zhang Y,  Friedman JM;
XX
DR   WPI; 2000-302788/26.
DR   P-PSDB; AAY87725.
XX
PT   Modifying body weight of an animal comprises administering mammalian
PT   obesity polypeptide obtained from humans and murine  -
XX
PS   Example 1; Column 99-102; 153pp; English.
XX
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CC   This invention describes a novel method for modifying body weight of
CC   an animal which comprises administering mammalian obesity (OB)
CC   polypeptide. The products of the invention have anorectic activity.
CC   The OB polypeptide at a dose of 5 mg/g/day in 300 micro litres of PBS
CC   was injected intraperitoneally into mice. Control mice were injected
CC   with PBS dialysate of the recombinant protein. The body weight of the
CC   mice was noted. The results shows that recombinant the OB polypeptide
CC   is capable of reducing a body weight and is found to be effective when
CC   it is administered daily. The OB polypeptide acts as a part of the
CC   signalling pathway by which adipose tissue communicates with the brain
CC   and other organs. (I) is useful for modulating body weight of an animal
CC   especially humans. This sequence encodes a murine OB protein described
CC   in the method of the invention.
XX
SQ   Sequence 2793 BP; 689 A; 653 C; 740 G; 711 T; 0 other;


  Query Match             33.7%;  Score 80.6;  DB 21;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 1.9e-15;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy        1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
            ||||||| ||||||  ||||||||||   ||    |    |||||||  ||  |||||
Db     1225 ctggttttgtttctattgtgactgactctatccaaacacgtttgcagcggcattgcc--- 1281

Qy       61 agtggatctccaaggaccaggttatttttaaaaagatttgtttttgtcaagtgtcatatgta 120
               ||| |      |     ||||   ||  ||||   |||||||||||||| |||||||
Db     1282 --gggagcataggctaggttattatcaaaagcagatgaatttttgtcaagtgtaatatgta 1339

Qy      121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
             | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db     1340 tctatgtgcacctgagggtagaggatgtgttagagggagggtgaaggatccggaa-gtgt 1398

Qy      181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
            | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db     1399 tctctgaattacatatgtgtggtaggcttttctgaaagggtgaggcatttt 1449


RESULT   9
AAF76943
ID   AAF76943 standard; cDNA; 2793 BP.
XX
AC   AAF76943;
XX
DT   21-MAY-2001  (first entry)
XX
DE   Murine leptin cDNA.
XX
KW   Murine; ob; leptin; antidiabetic; anorectic; anabolic;
     leptin transport; blood-brain barrier; adrenergic; neurotransmitter;
     cytokine; purinergic; glutaminergic; body weight; appetite;
KW   eating disorder; obesity; anorexia; diabetes; insulin resistance; ss.
XX
OS   Mus sp.
XX
PN   WO200113935-A2.
XX
PD   01-MAR-2001.
XX
PF   23-AUG-2000; 2000WO-US23110.
XX
PR   23-AUG-1999;   99US-0150300.
XX
PA   (TULA ) UNIV TULANE.
XX
PI   Banks WA;
XX
DR   WPI; 2001-257589/26.
DR   P-PSDB; AAB70127.
XX
PT   Modulating transport of leptin across the blood-brain barrier for
PT   modulating body weight and appetite in a mammal, involves administering
PT   adrenergic agonist or antagonist, neurotransmitter or cytokines -
XX
PS   Disclosure; Page 43-46; 50pp; English.
XX
CC   The present sequence encodes murine leptin. It is given in a
CC   specification relating to a method for modulating the transport of
CC   leptin across the blood-brain barrier of a mammal. The method involves
CC   administering one or more compositions selected from adrenergic
CC   agonists, adrenergic antagonists, neurotransmitters, cytokines, amino
CC   acids, opiate peptides, purinergic agonists, glutaminergic agonists or
CC   their metabolites. The compositions are useful for the manufacture of
CC   a medicament for modulating the transport of leptin across the
CC   blood-brain barrier, for modulating (reducing or increasing) body
CC   weight, and for modulating appetite in a mammal. They are also useful
CC   for treating eating disorders such as obesity, anorexia, type I and
CC   type II diabetes and insulin resistant pathologies.
XX
SQ   Sequence 2793 BP; 689 A; 653 C; 740 G; 711 T; 0 other;


  Query Match             33.7%;  Score 80.6;  DB 22;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 1.9e-15;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy        1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
            ||||||| ||||||  ||||||||||   ||    |    |||||||  ||  |||||
Db     1225 ctggttttgtttctattgtgactgactctatccaaacacgtttgcagcggcattgcc--- 1281

Qy       61 agtggatctccaaggaccaggttatttttaaaaagatttgtttttgtcaagtgtcatatgta 120
               ||| |      |     ||||   ||  ||||   |||||||||||||| |||||||
Db     1282 --gggagcataggctaggttattatcaaaagcagatgaatttttgtcaagtgtaatatgta 1339

Qy      121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
             | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db     1340 tctatgtgcacctgagggtagaggatgtgttagagggagggtgaaggatccggaa-gtgt 1398

Qy      181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
            | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db     1399 tctctgaattacatatgtgtggtaggcttttctgaaagggtgaggcatttt 1449


RESULT  10
AAV17090
ID   AAV17090 standard; DNA; 5917 BP.
XX
AC   AAV17090;
XX
DT   02-JUL-1998  (first entry)
XX
DE   Porcine adipocyte polypeptide leptin encoding DNA.
XX
KW   Porcine; adipocyte; leptin; pig; fat deposition; energy intake;
KW   metabolism; weight gain; ss.
XX
OS   Sus scrofa.
XX
FH   Key             Location/Qualifiers
FT   CDS             942..3756
FT                   /*tag= a
FT                   /product= "leptin"
FT                   /note= "contains an intron"
FT   exon            1..1085
FT                   /*tag= b
FT                   /number= 1
FT   intron          1086..3399
FT                   /*tag= c
FT                   /number= 1
FT   exon            3400..5917
FT                   /*tag= d
FT                   /number= 2
XX
PN   WO9804690-A1.
XX
PD   05-FEB-1998.
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XX
PF   17-JUL-1997;   97WO-US12483.
XX
PR   31-JUL-1996;   96US-0692922.
XX
PA   (PURD ) PURDUE RES FOUND.
PA   (PURI-) PURINA MILLS INC.
XX
PI   Bidwell CA,  Spurlock ME;
XX
DR   WPI; 1998-130682/12.
DR   P-PSDB; AAW49901.
XX
PT   New DNA encoding porcine adipocyte polypeptide - useful for, e.g.
PT   determining susceptibility to fat deposition and for controlling
PT   feed intake in pigs
XX
PS   Claim 4; Fig 1; 48pp; English.
XX
CC   The present sequence encodes porcine adipocyte polypeptide leptin.
CC   Measuring levels of leptin, or the nucleic acid encoding it, in
CC   biological fluids or tissues is used to determine the susceptibility of
CC   pigs to deposit fat. Similar measurements done in vitro on adipocytes in
CC   presence of a test compound are used to identify agents that can
CC   modulate fat deposition. Excessive fat deposition in pigs can be
CC   prevented, and energy intake, metabolism and weight gain controlled by
CC   treatment with leptin, antibodies against it or nucleic acids encoding
CC   it. The same results are achieved by altering expression of the leptin-
CC   encoding gene. Host cells containing leptin encoding nucleic acids are
CC   used for production of recombinant leptin and its encoding nucleic
CC   acids, or its fragments, can be used to isolate related sequences. Ab
CC   are also useful as immunoassay reagents for leptin or for affinity
CC   purification. Leptin can be administered by injection or orally
CC   (including consumption in genetically altered feeds). Use of leptin
CC   provides pigs with reduced levels of fat and allows matching of nutrient
CC   content of feed with nutritional requirements of the feed. The
CC   treatments can be applied to growing, finishing, lactating or pregnant
CC   pigs.
XX
SQ   Sequence 5917 BP; 1317 A; 1567 C; 1641 G; 1383 T; 9 other;

  Query Match             30.7%;  Score 73.4;  DB 19;  Length 5917;
  Best Local Similarity   59.4%;  Pred. No. 4.7e-13;
  Matches  142;  Conservative    0;  Mismatches   96;  Indels    1;  Gaps    1;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           |||| ||  ||||||||||||||||  ||| | |       |   |  |   |  ||||
Db    4366 ctggctttgtttctactgtgactgactttaaaactgcagcgtgtgcactggcatcgcctg 4425

Qy      61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
            | |||||||  |||| |||||||  | ||| |||||      |   |   |||||   ||
Db    4426 cgcggatctcgaagggccaggttctcttagaaagaagaagatgaactt-tgtcaggggtg 4484

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
           ||    | |  ||||    | |   ||  | |  | | |||    ||    | || | |
Db    4485 tgtacgcggagacaggaagtgtgttggtgggcggggcatggatccagaatgtgtatttct 4544

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
           | | |||   ||||||||||  ||| ||| ||||  | ||||| ||||| ||| ||||
Db    4545 tgtgtgatggacatttgtgtgaggggctctctggacagggtgaggtcattgtctcatct 4603

RESULT  11
ABL34358
ID   ABL34358 standard; DNA; 12237 BP.
XX
AC   ABL34358;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 2331.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 2331; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 12237 BP; 3050 A; 207 C; 3024 G; 5956 T; 0 other;

  Query Match             15.1%;  Score 36;  DB 24;  Length 12237;
  Best Local Similarity   51.9%;  Pred. No. 0.41;
  Matches   81;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy      80 ggttattttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggt 139
           |||| ||||||||||   |  ||| |   ||   |  ||    | |    |   || |||
Db    5847 ggtttttttaaaaagtaatagttttttttgtaaaaagtggttatattattattaagcggt 5906

Qy     140 ggggaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtg 199
           ||  | |||  |    |    | ||||  | | |    | | || |   |    | | |
Db    5907 ggatagtgtaagtttggggttgggaagatttttgggattatattgtagttttgttatttt 5966

Qy     200 tggtgggttctttggaaggagtgagatcatttttctt 235
           |||  || |   | |||||||||   | |||||  ||
Db    5967 gggttgggtgagtcgaaggagtgtttttatttttttt 6002


RESULT  12
ABL32161
ID   ABL32161 standard; DNA; 5314 BP.
XX
AC   ABL32161;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 134.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
```

```
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 134; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 5314 BP; 1212 A; 170 C; 1408 G; 2504 T; 20 other;


  Query Match             15.0%;  Score 35.8;  DB 24;  Length 5314;
  Best Local Similarity   53.1%;  Pred. No. 0.36;
  Matches   76;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy      41 tttgcaatggtgttgccctgagtggatctccaaggaccaggttattttaaaaagatttgt 100
           ||||   |   ||||    | ||||   |      |    | ||| ||| || | ||| ||
Db    3118 tttgattttaagttgtttggggtggggttgttgtgttgtgtttagtttgaatatattcgt 3177

       101 tttgtcaagtgtcatatgtaggtgtctgcacccaggggtggggaatgtttgggcagaagg 160
             |  | |   ||   || |  |||| || |   ||| ||  |||  |||| ||  |  ||
Db    3178 atgtttagacgtataatttgagtgtttgaaggtaggagttaggatggttttggaggttgg 3237

Qy     161 gagaaggatctagaatgtgtttt 183
           |    || |  || || | ||||
Db    3238 ggagtgggtggaggatttttttt 3260


RESULT  13
ABL33195
ID   ABL33195 standard; DNA; 14861 BP.
XX
AC   ABL33195;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 1168.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 1168; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 14861 BP; 3658 A; 228 C; 4018 G; 6955 T; 2 other;


  Query Match             14.4%;  Score 34.4;  DB 24;  Length 14861;
  Best Local Similarity   51.3%;  Pred. No. 1.4;
  Matches   80;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy      82 ttatttttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtgg 141
           |||||||  |    |||| ||||   || ||  |      |  |         | |  |
Db    6918 ttatttttattgtatttatttttagtaattggtaatatgtcggtttaaggggggtgtggga 6977

Qy     142 ggaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtgtg 201
           ||||  |||  ||  | | ||  | ||||  |    | | |||| ||| |   ||||||  ||
Db    6978 ggaaggttaggaaaaagggagggaggaagttagttttattttgtgagttgtatttgtttg 7037

Qy     202 gtgggttctttggaaggagtgagatcattttcttat 237
           | ||  | |||   |  ||  |     ||||  | |
Db    7038 ggggtgtttttttttattagaaaatgtttttttaattt 7073


RESULT  14
AAS61203
ID   AAS61203 standard; DNA; 14861 BP.
XX
AC   AAS61203;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Human gene regulation-associated gene oligonucleotide #158.
XX
KW   Human; Gene regulation-associated gene; severe combined immunodeficiency;
KW   cardiac damage; inflammatory response; Haemophilia; Werner syndrome;
KW   asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;
KW   renal disease; Preeclampsia; cardiac allograft vascular disease;
KW   colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
KW   immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
```

```
KW   nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200177375-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-EP03968.
XX
PR   06-APR-2000; 2000DE-1019058.
PR   07-APR-2000; 2000DE-1019173.
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;

DR   WPI; 2002-017470/02.
XX
PT   New nucleic acid sequences from chemically modified genes associated
PT   with gene regulation, useful for analysing cytosine methylations for
PT   diagnosis and therapy of diseases e.g. severe combined immunodeficiency
PT   disease -
XX
PS   Claim 1; SEQ ID No 162; 26pp; English.
XX
CC   The invention relates to 224 nucleic acid sequences comprising at least
CC   18 bases of a chemically pretreated gene associated with gene regulation
CC   selected from 43 known genes (or complementary sequences). The
CC   chemical pretreatment converts cytosine bases unmethylated at the
CC   5-position to uracil or another base with hybridisation behaviour
CC   dissimilar to cytosine, to enable analysis of cytosine methylations.
CC   The DNA sequences, oligomers (or sets/arrays) and method are
CC   useful in the diagnosis of diseases (or predisposition to diseases)
CC   associated with gene regulation and in therapy of such diseases, by
CC   enabling analysis of the cytosine methylation patterns of such genes,
CC   kits are provided. They are especially useful in diagnosis
CC   and therapy of e.g. severe combined immunodeficiency disease, cardiac
CC   disorders, haemophilia, solid tumours and cancer, Werner syndrome,
CC   asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease,
CC   preeclampsia, graft versus-host disease. The present sequence is a
CC   sequence included in the sequence data for this specification and is
CC   associated with the human gene regulation-associated genes.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 14861 BP; 3658 A; 228 C; 4018 G; 6955 T; 2 other;


  Query Match             14.4%;  Score 34.4;  DB 24;  Length 14861;
  Best Local Similarity   51.3%;  Pred. No. 1.4;
  Matches   80;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy      82 ttatttttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtgg 141
           ||||||| |    |||| ||||   || ||  |       |  |         | |  |
Db    6918 ttatttttattgtatttatttttagtaattggtaatatgtcggtttaaggggggtgtgtgga 6977

Qy     142 ggaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtgtg 201
           |||| ||| ||  | | ||  | ||||  |    | | |||| ||| |   |||||| ||
Db    6978 ggaaggttaggaaaaagggagggaggaagttagttttattttgtgagttgtatttgtttg 7037

Qy     202 gtgggttctttggaaggagtgagatcattttcttat 237
           | ||  | |||   |  ||  |     ||||  | |
Db    7038 ggggtgtttttttttattagaaaatgttttttaattt 7073


RESULT  15
AAN70097
ID   AAN70097 standard; DNA; 311 BP.
XX
AC   AAN70097;
XX
DT   17-APR-1991  (first entry)
XX
DE   Sequence of Ex promoter in E. coli expression plasmid
DE   pEAP7-delta-P.
XX
KW   Extracellular secretion; expression vector; ss.
XX
FH   Key             Location/Qualifiers
FT   -35_signal      44..49
FT                   /*tag=  a
FT   -10_signal      73..78
FT                   /*tag=  b
FT   RBS             150..155
FT                   /*tag=  c
FT   mRNA            85..169
FT                   /*tag=  d
FT   CDS             170..311
FT                   /*tag=  e
XX
PN   EP216080-A.
XX
PD   01-APR-1987.
XX
PF   30-JUL-1986;   86EP-0110534.
XX
PR   30-JUL-1985;   85JP-0168288.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
XX
PI   Horikoshi K,  Kudo T,  Kato C,  Kobayashi T;
XX
DR   WPI; 1987-087874/13.
XX
PT   New plasmid with DNA region inducing extracellular secretion of
PT   prod. - useful in transformed host microorganism for prodn. of
PT   enzymes, hormones, antiviral proteins etc.
XX
PS   Disclosure; Fig 3; 39pp; English.
XX
CC   Plasmid PEAP7-delta-P (claimed) contains a DNA region which is
CC   capable of inducing extracellular secretion of useful,
CC   physiologically active substances in transformed host,(designated K
CC   gene) and a promoter DNA gene which regulates expression of K gene
CC   (designated Ex promoter) and a genetic marker.  Mechanism of the
CC   extracellular secretion is believed to be that K gene and Ex
CC   promoter make the outer membrane of E. coli more permeable.
XX
SQ   Sequence 311 BP; 96 A; 41 C; 77 G; 97 T; 0 other;


  Query Match             14.3%;  Score 34.2;  DB 8;  Length 311;
  Best Local Similarity   58.3%;  Pred. No. 0.42;
  Matches   60;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       5 tttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctgagtg 64
             ||  || | || ||||| |||| | |||||||  | |||  |  ||| ||   || |  |
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Qy      65 gatctccaaggaccaggttattttaaaaagatttgttttgtca 107
             |    || ||   ||  |   |   | ||| |||||||| |
Db      87 tgtaatgaatgattgggagagggtgggatgatatgttttgtta 129


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Job time: 11123 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 13, 2002, 12:49:48 ; Search time 75.79 Seconds
(without alignments)
774.593 Million cell updates/sec

Title: US-09-437-458-17
Perfect score: 239
Sequence: 1 ctggtttcatttctactgtg.....gtgagatcattttcttatct 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

arched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		239	100.0	239	4	US-09-437-457-17	Sequence 17, Appl
2		80.6	33.7	2793	2	US-08-347-563A-1	Sequence 1, Appli
3		80.6	33.7	2793	3	US-08-485-942A-1	Sequence 1, Appli
4		80.6	33.7	2793	3	US-08-488-214A-1	Sequence 1, Appli
5		80.6	33.7	2793	3	US-08-488-208A-1	Sequence 1, Appli
6		80.6	33.7	2793	4	US-08-483-211A-1	Sequence 1, Appli
7		80.6	33.7	2793	4	US-08-488-223A-1	Sequence 1, Appli
8		73.4	30.7	5917	4	US-08-692-922-1	Sequence 1, Appli
9	c	29.8	12.5	2449	4	US-08-840-767-7	Sequence 7, Appli
10		29	12.1	5474	1	US-08-137-252-2	Sequence 2, Appli
11		28	11.7	3111	2	US-09-014-969-12	Sequence 12, Appl
12		27.8	11.6	824	2	US-08-922-170B-12	Sequence 12, Appl
13	c	27.8	11.6	3098	1	US-08-447-500-1	Sequence 1, Appli
14	c	27.8	11.6	3098	1	US-08-454-097-1	Sequence 1, Appli
15	c	27.8	11.6	3098	1	US-08-447-408-1	Sequence 1, Appli
16	c	27.8	11.6	3098	1	US-08-453-866-1	Sequence 1, Appli
17	c	27.8	11.6	3098	3	US-08-185-359-1	Sequence 1, Appli
18		27.6	11.5	1380	4	US-09-181-336-16	Sequence 16, Appl
19	c	27.4	11.5	90050	4	US-09-245-041-5	Sequence 5, Appli
20		27.2	11.4	5051	2	US-08-239-276-2	Sequence 2, Appli
21		27.2	11.4	5051	2	US-08-468-579B-2	Sequence 2, Appli
22		27.2	11.4	5051	3	US-08-468-577B-2	Sequence 2, Appli
23	c	27.2	11.4	12720	1	US-08-403-866-11	Sequence 11, Appl
24		27	11.3	2508	4	US-09-347-833-1	Sequence 1, Appli
25	c	27	11.3	8600	4	US-09-457-708-1	Sequence 1, Appli
26	c	26.8	11.2	1693	6	5169835-3	Patent No. 5169835
27		26.6	11.1	935	4	US-09-328-111-626	Sequence 626, App
28		26.6	11.1	946	3	US-09-188-930-258	Sequence 258, App
29		26.6	11.1	2328	1	US-08-688-649-38	Sequence 38, Appl
30		26.6	11.1	2328	4	US-09-715-524B-1	Sequence 1, Appli
31		26.6	11.1	3499	1	US-07-966-278-2	Sequence 2, Appli
32		26.6	11.1	3499	1	US-08-424-921-2	Sequence 2, Appli
33		26.6	11.1	3499	2	US-08-556-355A-2	Sequence 2, Appli
34		26.6	11.1	3499	2	US-07-803-627A-2	Sequence 2, Appli
35	c	26.6	11.1	4823	2	US-08-457-254-5	Sequence 5, Appli
36	c	26.6	11.1	4823	2	US-08-484-257-20	Sequence 20, Appl
37	c	26.6	11.1	4823	3	US-08-999-927-5	Sequence 5, Appli
38	c	26.6	11.1	4823	4	US-08-461-819-5	Sequence 5, Appli
39	c	26.6	11.1	4823	5	PCT-US94-08806-28	Sequence 28, Appl
40	c	26.6	11.1	4823	5	PCT-US95-01829-5	Sequence 5, Appli
41	c	26.6	11.1	4823	5	PCT-US95-16626-5	Sequence 5, Appli
42	c	26.4	11.0	1728	2	US-08-417-495-1	Sequence 1, Appli
43	c	26.4	11.0	1728	2	US-08-284-391B-1	Sequence 1, Appli
44	c	26.4	11.0	1728	4	US-09-218-950-1	Sequence 1, Appli
45	c	26.4	11.0	1728	5	PCT-US92-01785-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-437-457-17
; Sequence 17, Application US/09437457
; Patent No. 6273893
; GENERAL INFORMATION:
; APPLICANT: Giordano, Anthony
; APPLICANT: Xavier, Ashish
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
; TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
; FILE REFERENCE: 50093/014001
; CURRENT APPLICATION NUMBER: US/09/437,457
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-437-457-17

Query Match 100.0%; Score 239; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.6e-69;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60

Qy      61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180

Qy     181 ttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
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RESULT 2
US-08-347-563A-1
; Sequence 1, Application US/08347563A
; Patent No. 5935810
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC

```
;    TITLE OF INVENTION:  ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREO
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/347,563A
;      FILING DATE:  No. 5935810ember 30, 1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/292,345
       FILING DATE:  August 17, 1994
       CLASSIFICATION:  514
     ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-087 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2793 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  Murine ob cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Murine
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  57..560
US-08-347-563A-1


  Query Match             33.7%;  Score 80.6;  DB 2;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 4e-17;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||||| |||||| |||||||||    ||    |    ||||||| ||  |||||
Db    1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
             ||| |       |     ||||   ||  ||||   |||||||||||| |||||||
Db    1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
             | | ||||||   |||| | | |||| |  |   | |||| ||||||||  ||| ||||
Db    1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
           | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db    1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT   3
US-08-485-942A-1
; Sequence 1, Application US/08485942A
; Patent No., 6048837
;  GENERAL INFORMATION:
;    APPLICANT:  JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
;    APPLICANT:  MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BI
;    TITLE OF INVENTION:  OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
;    TITLE OF INVENTION:  AMENDED)
;    NUMBER OF SEQUENCES:  99
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,942A
;      FILING DATE:  JUNE 7, 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/438,431
;      FILING DATE:  May 10, 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/347,563
;      FILING DATE:  No. 6048837ember 30, 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/292,345
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-087 CIP 2F
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2793 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  Murine ob cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Murine
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  57..560
US-08-485-942A-1


  Query Match             33.7%;  Score 80.6;  DB 3;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 4e-17;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||||| |||||| |||||||||    ||    |    ||||||| ||  |||||
Db    1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
             ||| |       |     ||||   ||  ||||   |||||||||||| |||||||
Db    1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
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           | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT   4
US-08-488-214A-1
; Sequence 1, Application US/08488214A
; Patent No. 6124439
;  GENERAL INFORMATION:
;    APPLICANT:  JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
;    APPLICANT:  MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE
;    TITLE OF INVENTION:  OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
;    TITLE OF INVENTION:  (AS AMENDED)
;    NUMBER OF SEQUENCES:  99
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,214A
;      FILING DATE:  JUNE 7, 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/438,431
;      FILING DATE:  May 10, 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/347,563
;      FILING DATE:  No. 6124439ember 30, 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/292,345
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-087 CIP 2D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2793 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  Murine ob cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Murine
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  57..560
US-08-488-214A-1


  Query Match             33.7%;  Score 80.6;  DB 3;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 4e-17;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
          |||||||  ||||||  |||||||||   ||    |   |||||||  ||  |||||
Db   1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy     61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
            ||| |       |     ||||   ||  ||||   ||||||||||||| |||||||
Db   1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT   5
US-08-488-208A-1
; Sequence 1, Application US/08488208A
; Patent No. 6124448
;  GENERAL INFORMATION:
;    APPLICANT:  THE ROCKEFELLER UNIVERSITY
;    TITLE OF INVENTION:  MODULATORS OF BODY WEIGHT, CORRESPONDING
;    TITLE OF INVENTION:  NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
;    TITLE OF INVENTION:  USES THEREOF
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,208A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/485,943
;      FILING DATE:  June 7, 1995
;      APPLICATION NUMBER:  08/438,431
;      FILING DATE:  May 10, 1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/347,563
;      FILING DATE:  No. 6124448ember 30, 1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/292,345
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-087 CIP2I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2793 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
```

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  Murine ob cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Murine
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  57..560
US-08-488-208A-1


  Query Match            33.7%;  Score 80.6;  DB 3;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 4e-17;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
          ||||||| |||||| |||||||||   ||    |    |||||||  ||  |||||
Db   1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

       61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
            ||| |      |     ||||   ||  ||||   |||||||||||||| |||||||
Db   1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT   6
US-08-483-211A-1
; Sequence 1, Application US/08483211A
; Patent No. 6309853
;  GENERAL INFORMATION:
;    APPLICANT:  THE ROCKEFELLER UNIVERSITY
;    TITLE OF INVENTION:  MODULATORS OF BODY WEIGHT, CORRESPONDING
;    TITLE OF INVENTION:  NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
;    TITLE OF INVENTION:  USES THEREOF
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,211A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/485,943
;      FILING DATE:  June 7, 1995
;      APPLICATION NUMBER:  08/438,431
;      FILING DATE:  May 10, 1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/347,563
;      FILING DATE:  No. 6309853ember 30, 1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/292,345
;      FILING DATE:  August 17, 1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-087 CIP2I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2793 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  Murine ob cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Murine
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  57..560
US-08-483-211A-1


  Query Match            33.7%;  Score 80.6;  DB 4;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 4e-17;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
          ||||||| |||||| |||||||||   ||    |    |||||||  ||  |||||
Db   1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy     61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
            ||| |      |     ||||   ||  ||||   |||||||||||||| |||||||
Db   1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT   7
US-08-488-223A-1
; Sequence 1, Application US/08488223A
; Patent No. 6350730
;  GENERAL INFORMATION:
;       APPLICANT: THE ROCKEFELLER UNIVERSITY
;       TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
;                           ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES
;       NUMBER OF SEQUENCES: 98
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Klauber & Jackson
;            STREET: 411 Hackensack Avenue
;            CITY: Hackensack
;            STATE: New Jersey
;            COUNTRY: USA
;            ZIP: 07601
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/488,223A
;            FILING DATE: 07-Jun-1995
;            CLASSIFICATION: <Unknown>
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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/485,943
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/347,563
;            FILING DATE: No. 6350730ember 30, 1994
;            APPLICATION NUMBER: 08/292,345
;            FILING DATE: August 17, 1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Jackson Esq., David A.
;            REGISTRATION NUMBER: 26,742
;            REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 201 487-5800
;            TELEFAX: 201 343-1684
;            TELEX: 133521
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2793 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;            DESCRIPTION: Murine ob cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Murine
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  57..560
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-488-223A-1


  Query Match             33.7%;  Score 80.6;  DB 4;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 4e-17;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           |||||||  ||||||  |||||||||    ||     |    |||||||  ||  |||||
Db    1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
             ||| |.       |     ||||   ||  ||||   |||||||||||||| |||||||
Db    1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

       121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
             | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db    1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
           | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db    1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT   8
US-08-692-922-1
; Sequence 1, Application US/08692922
; Patent No. 6277592
;  GENERAL INFORMATION:
;    APPLICANT:  Bidwell, Christopher A.
;    APPLICANT:  Spurlock, Michael E.
;    TITLE OF INVENTION:  PORCINE LEPTIN PROTEIN, NUCLEIC ACID
;    TITLE OF INVENTION:  SEQUENCES CODING THEREFOR AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WHYTE HIRSCHBOECK DUDEK S.C.
;      STREET:  Suite 2100 111 East Wisconsin Avenue
;      CITY:  Milwaukee
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/692,922
;      FILING DATE:  31-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shaw, Melissa A.
;      REGISTRATION NUMBER:  38,301
;      REFERENCE/DOCKET NUMBER:  PM-8935
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  414-273-2100
;      TELEFAX:  414-223-5000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5917 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(942..1085, 3400..3753)
US-08-692-922-1


  Query Match             30.7%;  Score 73.4;  DB 4;  Length 5917;
  Best Local Similarity   59.4%;  Pred. No. 1.3e-14;
  Matches  142;  Conservative    0;  Mismatches   96;  Indels    1;  Gaps    1;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           |||| ||  ||||||||||||||||  ||| | |       |    |  |   | ||||
Db    4366 CTGGCTTTGTTTCTACTGTGACTGACTTTAAAACTGCAGCGTGTGCACTGGCATCGCCTG 4425

Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
           | |||||||| |||| |||||||  | ||| |||||       |   |  |||||   ||
Db    4426 CGCGGATCTCGAAGGGCCAGGTTCTCTTAGAAAGAAGAAGATGAACTT-TGTCAGGGGTG 4484

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
           ||    | |  ||||    | |   ||  | |  | | |||    ||    | || | |
Db    4485 TGTACGCGGAGACAGGAAGTGTGTTGGTGGGCGGGGCATGGATCCAGAATGTGTATTTCT 4544

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
           | | |||   |||||||||||  ||| ||| ||||  | |||||  ||||| ||| ||||
Db    4545 TGTGTGATGGACATTTGTGTGAGGGGCTCTCTGGACAGGGTGAGGTCATTGTCTCATCT 4603


RESULT   9
US-08-840-767-7/c
; Sequence 7, Application US/08840767B
; Patent No. 6255464
; GENERAL INFORMATION:
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth W.
;  APPLICANT: Riggins, Gregory J.
;  APPLICANT: Thiagalingam, Sam
;  TITLE OF INVENTION: MAD-Related Genes in the Human
;  FILE REFERENCE: 01107.05548
;  CURRENT APPLICATION NUMBER: US/08/840,767B
;  CURRENT FILING DATE: 1997-04-16
;  EARLIER APPLICATION NUMBER: 60/015,823
;  EARLIER FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 2449
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-840-767-7
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  Query Match            12.5%;  Score 29.8;  DB 4;  Length 2449;
  Best Local Similarity   47.6%;  Pred. No. 1.8;
  Matches   88;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy      55 gccctgagtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtca 114
           | |||   || | ||| |||     || ||    || || |  |     || ||  ||||
Db     356 GACCTTCCTGTAACTCAAAGTCAGTGGCTACCGAAAGAACAGATCACAGGTGAAACGTCA 297

Qy     115 tatgtaggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctaga 174
           ||   ||||        || |   || |   | | | ||   |  | ||   |  |||
Db     296 TACACAGGTCCTAAGCACCTGCCCAGGCGGCCGCTCGAGCCCTATAGTGAGTCACGTAGT 237

Qy     175 atgtgttttctgaataacatttgtgtggtgggttctttggaaggagtgagatcatttttct 234
           ||| || || |||   |     || |  |  || || || |     | |  |  ||||
Db     236 ATGGGTGTTATGAGATATGAGAGTTTATTATGTCCTATGTAGTAGATCATTTTTTTTTTC 177

Qy     235 tatct 239
           |  ||
Db     176 TGACT 172


  :ULT  10
  -08-137-252-2
; Sequence 2, Application US/08137252
; Patent No. 5480774
;  GENERAL INFORMATION:
;    APPLICANT:  Hew, Choy L.
;    APPLICANT:  Du, Shoa J.
;    TITLE OF INVENTION:  DETERMINATION OF GENOMIC SEX IN
;    TITLE OF INVENTION:  SALMONIDS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,252
;      FILING DATE:  14-OCT-1993
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Kenneth A.
       REGISTRATION NUMBER:  31,677
       REFERENCE/DOCKET NUMBER:  16252-0002
,    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5474 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Chinook Salmon
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..5474
;      OTHER INFORMATION:  /standard_name= "Nucleotide
;      OTHER INFORMATION:  Sequence of the Chinook Salmon GH Pseudogene"
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1349..1414
;    FEATURE:
; -  ,  NAME/KEY:  intron
;      LOCATION:  1415..1810
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1811..1950
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1951..2086
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2087..2203
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  2204..2660
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2661..2816
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  2817..4769
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  4770..4853
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  4854..5003
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  5004..5474
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  134..399
;      OTHER INFORMATION:  /note= "The 266 bp homologous
;      OTHER INFORMATION:  region shared with GH-I in their 5' flanking
;      OTHER INFORMATION:  regions."
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  4836..4838
;      OTHER INFORMATION:  /note= "The premature stop codon in
;      OTHER INFORMATION:  exon 5."
US-08-137-252-2


  Query Match            12.1%;  Score 29;  DB 1;  Length 5474;
  Best Local Similarity   52.0%;  Pred. No. 4.5;
  Matches   65;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy     115 tatgtaggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctaga 174
           | |||  |||  || | |    | |     ||  |     |||    ||| |  | |
Db    1050 TCTGTGTGTGAGTGTAACTTTTGTTCATTCATTATGTCCTAGACAACAGAGGTTTGTTTT 1109

Qy     175 atgtgttttctgaataacatttgtgtggtgggttctttggaaggagtgagatcatttttct 234
           | ||| || |||     ||||||   ||  ||| ||| | ||||| |  | || || ||
Db    1110 GTATGTGTTTTGACCCTAATTTGTCAAGTAAGTTTTTTTGTAGGAGAGTCACCAGTTCCT 1169

Qy     235 tatct 239
           | ||
Db    1170 GAACT 1174


RESULT  11
US-09-014-969-12
; Sequence 12, Application US/09014969
; Patent No. 5965397
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John M.
;    APPLICANT:  LaVallie, Edward R.
;    APPLICANT:  Racie, Lisa A.
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    APPLICANT:  Agostino, Michael J.
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
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;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/014,969
;      FILING DATE:
;      CLASSIFICATION:
     ATTORNEY/AGENT INFORMATION:
       NAME:  Sprunger, Suzanne A.
;      REGISTRATION NUMBER:  41,323
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3111 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-014-969-12


  Query Match             11.7%;  Score 28;  DB 2;  Length 3111;
  Best Local Similarity   49.3%;  Pred. No. 7.6;
  Matches   73;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy      72 aaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcac 131
           |||| | |  |   ||  | | | || ||     | || || | ||       |||||
Db    2636 ATGGAACTGCCTGGATTTTATACAGTTATTAAAGGATGTCTCTTTTGCTTTAAACTGCAT 2695

Qy     132 ccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataa 191
             | |    | |  || |  || ||| |              | | |||| | |||   ||
Db    2696 GCTGCCAAGTGCCATTTGGGGTCAGCATCCTCGTTTCAACACAGTGTGCTCTCTAGTTAT 2755

      192 catttgtgtggtgggttctttggaagga 219
          ||| |||   |||||||||  |  |  ||
Db    2756 CATGTGTAACGTGGGTTCTGTTTAGCGA 2783


RESULT  12
US-08-922-170B-12
; Sequence 12, Application US/08922170B
; Patent No. 5968822
;  GENERAL INFORMATION:
;    APPLICANT:  Iris Pecker, Israel Vlodavsky and Elena
;    APPLICANT:  Feinstein
;    TITLE OF INVENTION:  POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
;    TITLE OF INVENTION:  HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
;    TITLE OF INVENTION:  SAME IN TRANSDUCED CELLS
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark M. Friedman c/o Robert Sheinbein
;      STREET:  2940 Birchtree lane
;      CITY:  Silver Spring
;      STATE:  Maryland
;      COUNTRY:  United States of America
;      ZIP:  20906
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 megabyte, 3.5" microdisk
;      COMPUTER:  Twinhead* Slimnote-890TX
;      OPERATING SYSTEM:  MS DOS version 6.2,
;      OPERATING SYSTEM:  Windows version 3.11
;      SOFTWARE:  Word for Windows version 2.0 converted to
;      SOFTWARE:  an ASCI file
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/922,170B
;      FILING DATE:  2 SEP 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Friedmam, Mark M.
;      REGISTRATION NUMBER:  33,883
;      REFERENCE/DOCKET NUMBER:  910/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  972-3-5625553
;      TELEFAX:  972-3-5625554
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  824
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-922-170B-12


  Query Match             11.6%;  Score 27.8;  DB 2;  Length 824;
  Best Local Similarity   47.4%;  Pred. No. 5.2;
  Matches   83;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy       9 atttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctgagtggatc 68
           | | | |   |  ||| |  || || | | |    |  ||   ||  |||||||   |
Db     603 AATGCCAAAATCGCTGCTTGTATATGAAAATAAAAGGCATACGGTACCCCTGAGACAAAA 662

Qy      69 tccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctg 128
             || |||     ||||||   |||| |      | ||  ||      |  |   || |
Db     663 GCCGAGGGGGGTGTTATTCATAAAACAAAACCCTAGTTTAGGAGGCCACCTCCTTGCCGA 722

Qy     129 cacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgtttt 183
             |||| | |  || | | | ||| | |    || | |  |  | |||| | |
Db     723 GTTCCAGAGCTTCGGGAGGGTGGGGTACACTTCAGTATTACATTCAGTGTGGTGT 777


RESULT  13
US-08-447-500-1/c
; Sequence 1, Application US/08447500
; Patent No. 5627064
;  GENERAL INFORMATION:
;    APPLICANT:  Hoekstra, Merl F.
;    TITLE OF INVENTION:  PROTEIN KINASES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  1880 Century Park East, Suite 500
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,500
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/008,001
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wetherell Ph.D., John R.
```

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;       REGISTRATION NUMBER:  31,678
;       REFERENCE/DOCKET NUMBER:  PD-2458
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 455-5100
;       TELEFAX:  (619) 455-5110
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3098 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     IMMEDIATE SOURCE:
;       CLONE:  Protein Kinase
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  879..2360
US-08-447-500-1


 Query Match             11.6%;  Score 27.8;  DB 1;  Length 3098;
  Best Local Similarity   50.4%;  Pred. No. 8.9;
  Matches   68;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy      83 tattttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtggg 142
           | ||||||  | || | |||   |   || | |||  |||    | |      || | |
Db     361 TCTTTTAATTATATCTCTTTATACGCATGCCGTATCGAGGACAATACCGAATTGGTTTAG 302

Qy     143 gaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtgtgg 202
             | || |   | ||   ||   ||| || |||  || || |  ||   | | ||||
Db     301 ATCTTTTAGTATACAATTAAGGGAGATATAAAATTGGTGTTGTTGATGTTACTAGTGTTA 242

Qy     203 tgggttctttggaag 217
           | | |   |  ||||
Db     241 TTGATAAATAAGAAG 227


RESULT  14
US-08-454-097-1/c
; Sequence 1, Application US/08454097
; Patent No. 5686412
;  GENERAL INFORMATION:
;    APPLICANT:  Hoekstra, Merl F.
;    TITLE OF INVENTION:  Protein Kinases
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive, 6300 Sears Tower
;      CITY:  Chicago
       STATE:  Illinois
       COUNTRY:  USA
,      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/454,097
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/185,359
;      FILING DATE:  21-JAN-1994
;      APPLICATION NUMBER:  US 08/008,001
;      FILING DATE:  21-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/728,783
;      FILING DATE:  03-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5686412and, Greta E.
;      REGISTRATION NUMBER:  35,302
; -    REFERENCE/DOCKET NUMBER:  27866/31853
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3098 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  Protein Kinase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  879..2360
US-08-454-097-1


  Query Match             11.6%;  Score 27.8;  DB 1;  Length 3098;
  Best Local Similarity   50.4%;  Pred. No. 8.9;
  Matches   68;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy      83 tattttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtggg 142
           | ||||||  | || | |||   |   || | |||  |||    | |      || | |
Db     361 TCTTTTAATTATATCTCTTTATACGCATGCCGTATCGAGGACAATACCGAATTGGTTTAG 302

Qy     143 gaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtgtgg 202
             | || |   | ||   ||   ||| || |||  || || |  ||   | | ||||
Db     301 ATCTTTTAGTATACAATTAAGGGAGATATAAAATTGGTGTTGTTGATGTTACTAGTGTTA 242

Qy     203 tgggttctttggaag 217
           | | |   |  ||||
Db     241 TTGATAAATAAGAAG 227


RESULT  15
US-08-447-408-1/c
; Sequence 1, Application US/08447408
; Patent No. 5705377
;  GENERAL INFORMATION:
;    APPLICANT:  Hoekstra, Merl F.
;    TITLE OF INVENTION:  TYROSINE KINASE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Spensley Horn Jubas & Lubitz
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,408
;      FILING DATE:  03-JUL-1991
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/728,783
;      FILING DATE:  03-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wetherell Ph.D., John R.
;      REGISTRATION NUMBER:  31,678
;      REFERENCE/DOCKET NUMBER:  PD-1318
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 455-5100
;      TELEFAX:  (619) 455-5110
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3098 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  Tyrosine Kinase
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  879..2364
US-08-447-408-1


  Query Match           11.6%;  Score 27.8;  DB 1;  Length 3098;
  Best Local Similarity  50.4%;  Pred. No. 8.9;
  Matches   68;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy      83 tattttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtggg 142
           | |||||| | || | |||   |   || | |||  |||    | |      || | |
Db     361 TCTTTTAATTATATCTCTTTATACGCATGCCGTATCGAGGACAATACCGAATTGGTTTAG 302

Qy     143 gaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtgtgg 202
             | || |   | ||   ||   ||| || |||  || || |  ||   | | ||||
Db     301 ATCTTTTAGTATACAATTAAGGGAGATATAAAATTGGTGTTGTTGATGTTACTAGTGTTA 242

Qy     203 tgggttctttggaag 217
           | | |   |  ||||
Db     241 TTGATAAATAAGAAG 227


Search completed: June 13, 2002, 15:19:07
Job time: 8959 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 13, 2002, 12:49:48 ; Search time 1868.55 Seconds
(without alignments)
2676.644 Million cell updates/sec

Title: US-09-437-458-17
Perfect score: 239
Sequence: 1 ctggtttcatttctactgtg.....gtgagatcattttcttatct 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

arched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	239	100.0	239	6	AR164465	AR164465 Sequence
2	239	100.0	3426	6	AX003702	AX003702 Sequence
3	239	100.0	3426	6	AX331545	AX331545 Sequence
4	239	100.0	3426	9	HSU43653	U43653 Human obese
5	239	100.0	4522	9	D63708S3	D63710 Human ob ge
6	239	100.0	4522	11	G31731	G31731 sWSS2619 Er
7	239	100.0	163549	9	AC018635	AC018635 Homo sapi
8	138	57.7	2935	4	AB041360	AB041360 Felis cat
9	134.2	56.2	1076	4	AF310264	AF310264 Ovis arie
10	130	54.4	2925	4	AB020986	AB020986 Canis fam
11	130	54.4	2925	6	E59801	E59801 Canine obsi
12	80.6	33.7	2793	6	AR175617	AR175617 Sequence
13	80.6	33.7	2793	6	AX088104	AX088104 Sequence
14	80.6	33.7	2793	10	MMU18812	U18812 Mus musculu
c 15	80.6	33.7	214257	2	AC072048	AC072048 Mus muscu
16	80	33.5	3113	4	AF026976	AF026976 Sus scrof
17	80	33.5	3277	4	AF052691	AF052691 Sus scrof
18	73.4	30.7	5920	4	SSU66254	U66254 Sus scrofa
19	72.6	30.4	4067	4	BTU50365	U50365 Bos taurus
20	51.8	21.7	155907	2	AC096035	AC096035 Rattus no
21	40.4	16.9	38860	9	HS27N19	AL132818 Homo sapi
22	40.4	16.9	151675	9	AP000470	AP000470 Homo sapi
c 23	40.4	16.9	178534	2	AC027203	AC027203 Homo sapi
24	40.4	16.9	340000	9	AP001689	AP001689 Homo sapi
c 25	38.8	16.2	178151	9	AL136123	AL136123 Human DNA
c 26	36.2	15.1	166510	9	AC087806	AC087806 Papio cyn
27	36.2	15.1	167077	2	AC091093	AC091093 Papio cyn
28	36.2	15.1	174132	2	AC095090	AC095090 Rattus no
c 29	36.2	15.1	180267	2	AC094608	AC094608 Rattus no
30	36	15.1	12237	6	AX347260	AX347260 Sequence
c 31	36	15.1	134939	2	AC025485	AC025485 Homo sapi
c 32	36	15.1	149739	2	AC099366	AC099366 Rattus no
33	36	15.1	175108	2	AC031982	AC031982 Homo sapi
34	36	15.1	176085	2	AL590309	AL590309 Homo sapi
c 35	36	15.1	187863	9	AL589740	AL589740 Human DNA
36	35.8	15.0	5314	6	AX281268	AX281268 Sequence
37	35.8	15.0	5314	6	AX345063	AX345063 Sequence
c 38	35.8	15.0	101255	2	AC078780_3	Continuation (4 of
39	35.8	15.0	143113	8	AP000559	AP000559 Oryza sat
40	35.6	14.9	167050	2	AC099097	AC099097 Rattus no
c 41	35.4	14.8	128764	2	AC103200	AC103200 Rattus no
c 42	35.4	14.8	191119	9	AC009957	AC009957 Homo sapi
c 43	35	14.6	73397	2	AC101427	AC101427 Mus muscu
c 44	35	14.6	156604	2	AC069371	AC069371 Homo sapi
c 45	35	14.6	175165	2	AP002780	AP002780 Homo sapi

ALIGNMENTS

RESULT 1
AR164465
LOCUS AR164465 239 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 17 from patent US 6273893.
ACCESSION AR164465
VERSION AR164465.1 GI:16237505
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 239)
AUTHORS McAllen,J. III, Overaker,D.W. and Cooper,K.L.
TITLE Absorbable rivet/pin applier for use in surgical procedures
JOURNAL Patent: US 6273893-A 17 14-AUG-2001;
FEATURES Location/Qualifiers
source 1. .239
/organism="unknown"
BASE COUNT 54 a 32 c 68 g 85 t
ORIGIN

Query Match 100.0%; Score 239; DB 6; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.4e-62;

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Db      1 CTGGTTTCATTTCTACTGTGACTGATGTTACATCACAGTGTTTGCAATGGTGTTGCCCTG 60

Qy     61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
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Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
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Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
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Db    181 TTTCTGAATAACATTTGTGTGGTGGGTTCTTTGGAAGGAGTGAGATCATTTTCTTATCT 239


RESULT   2
AX003702
LOCUS       AX003702                3426 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 4 from Patent WO9925824.
ACCESSION   AX003702
VERSION     AX003702.1  GI:9927488
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3426)
  AUTHORS   Issad,T. and Camoin,L.
  TITLE     Cdna sequence coding for a mutated leptin and applications
  JOURNAL   Patent: WO 9925824-A 4 27-MAY-1999;
            ISSAD TARIK (FR); CAMOIN LUC (FR)
FEATURES             Location/Qualifiers
     source          1. .3426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      887 a    798 c    920 g    821 t
ORIGIN


  Query Match           100.0%;  Score 239;  DB 6;  Length 3426;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-62;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   1262 CTGGTTTCATTTCTACTGTGACTGATGTTACATCACAGTGTTTGCAATGGTGTTGCCCTG 1321

Qy     61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
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Db   1322 AGTGGATCTCCAAGGACCAGGTTATTTTAAAAAGATTTGTTTTGTCAAGTGTCATATGTA 1381

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
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Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
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Db   1442 TTTCTGAATAACATTTGTGTGGTGGGTTCTTTGGAAGGAGTGAGATCATTTTCTTATCT 1500


RESULT   3
AX331545
LOCUS       AX331545                3426 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 2054 from Patent WO0194629.
ACCESSION   AX331545
VERSION     AX331545.1  GI:18122179
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 2054 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3426
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                     /db_xref="taxon:9606"
BASE COUNT      887 a    799 c    920 g    820 t
ORIGIN


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  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   1322 AGTGGATCTCCAAGGACCAGGTTATTTTAAAAAGATTTGTTTTGTCAAGTGTCATATGTA 1381

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
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Db   1382 GGTGTCTGCACCCAGGGGTGGGGAATGTTTGGGCAGAAGGGAGAAGGATCTAGAATGTGT 1441

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
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Db   1442 TTTCTGAATAACATTTGTGTGGTGGGTTCTTTGGAAGGAGTGAGATCATTTTCTTATCT 1500


RESULT   4
HSU43653
LOCUS       HSU43653                3426 bp    mRNA    linear   PRI 14-MAR-1996
DEFINITION  Human obese protein (ob) mRNA, complete cds.
ACCESSION   U43653
VERSION     U43653.1  GI:1226243
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3426)
  AUTHORS   Gong,D.W., Bi,S., Pratley,R.E. and Weintraub,B.D.
  TITLE     Genomic structure and promoter analysis of the human obese gene
  JOURNAL   J. Biol. Chem. 271 (8), 3971-3974 (1996)
  MEDLINE   96223958
REFERENCE   2  (bases 1 to 3426)
  AUTHORS   Gong,D.-W.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-1995) Da-Wei Gong, Molecular and Cellular
            Endocrinology Branch, NIDDK/NIH, Bldg10/Rm8D14, 10 Center Drive
            MSC1822, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .3426
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                     /db_xref="taxon:9606"
                     /chromosome="7"
     gene            1. .3426
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     CDS             57. .560
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                     /protein_id="AAC50400.1"
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                     /translation="MHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTLIKTIVTRIND
                     ISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLE
                     NLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYSTEVVALSRLQGSLQDMLWQ
                     LDLSPGC"
BASE COUNT      887 a    799 c    920 g    820 t
ORIGIN


  Query Match           100.0%;  Score 239;  DB 9;  Length 3426;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-62;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 CTGGTTTCATTTCTACTGTGACTGATGTTACATCACAGTGTTTGCAATGGTGTTGCCCTG 1321

Qy     61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
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Db   1322 AGTGGATCTCCAAGGACCAGGTTATTTTAAAAAGATTTGTTTTGTCAAGTGTCATATGTA 1381

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382 GGTGTCTGCACCCAGGGGTGGGGAATGTTTGGGCAGAAGGGAGAAGGATCTAGAATGTGT 1441

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442 TTTCTGAATAACATTTGTGTGGTGGGTTCTTTGGAAGGAGTGAGATCATTTTCTTATCT 1500


RESULT   5
D63708S3
LOCUS       D63708S3                4522 bp    DNA     linear   PRI 14-APR-2000
DEFINITION  Human ob gene, exon 3 and complete cds.
ACCESSION   D63710
VERSION     D63710.1  GI:1071653
KEYWORDS    obese gene; ob protein.
SEGMENT     3 of 3
SOURCE      Homo sapiens leukocyte DNA, clone_lib:lambda EMBL3 (CLONETECH)
            clone:OB1-8.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4522)
  AUTHORS   Isse,N., Ogawa,Y., Tamura,N., Masuzaki,H., Mori,K., Okazaki,T.,
            Satoh,N., Shigemoto,M., Yoshimasa,Y., Nishi,S., Hosada,K.,
            Inazawa,J. and Nakao,K.
  TITLE     Structural organization and chromosomal assignment of the human
            obese gene
  JOURNAL   J. Biol. Chem. 270 (46), 27728-27733 (1995)
  MEDLINE   96070903
REFERENCE   2  (bases 1 to 4522)
  AUTHORS   Ogawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-1995) Yoshihiro Ogawa, Kyoto University Graduate
            School of Medicine, Dept. of Medicine and Clinical Science; 54
            Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan
            (Tel:075-751-3173, Fax:075-771-9452)
FEATURES             Location/Qualifiers
     source          1. .4522
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                     /db_xref="taxon:9606"
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                     /map="7q31.3"
                     /clone="OB1-8"
                     /cell_type="leukocyte"
                     /clone_lib="lambda EMBL3 (CLONETECH)"
     gene            join(D63708.1:173. .201,D63709.1:31. .202,31. .4069)
                     /gene="ob"
     CDS             join(D63709.1:59. .202,31. .390)
                     /gene="ob"
                     /standard_name="obese"
                     /codon_start=1
                     /product="ob protein"
                     /protein_id="BAA09839.1"
                     /db_xref="GI:1407583"
                     /translation="MHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTLIKTIVTRIND
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                     LDLSPGC"
     intron          <1. .30
                     /gene="ob"
                     /number=2
     exon            31. .4069
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                     /standard_name="obese"
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BASE COUNT     1189 a   1032 c   1177 g   1124 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 5e-62;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   1092 CTGGTTTCATTTCTACTGTGACTGATGTTACATCACAGTGTTTGCAATGGTGTTGCCCTG 1151

Qy     61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
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Db   1152 AGTGGATCTCCAAGGACCAGGTTATTTTAAAAAGATTTGTTTTGTCAAGTGTCATATGTA 1211

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
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Db   1212 GGTGTCTGCACCCAGGGGTGGGGAATGTTTGGGCAGAAGGGAGAAGGATCTAGAATGTGT 1271

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
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Db   1272 TTTCTGAATAACATTTGTGTGGTGGGTTCTTTGGAAGGAGTGAGATCATTTTCTTATCT 1330


RESULT   6
G31731
LOCUS       G31731                  4522 bp    DNA     linear   STS 28-SEP-1998
DEFINITION  sWSS2619 Eric D. Green Homo sapiens STS genomic, sequence tagged
            site.
ACCESSION   G31731
VERSION     G31731.1  GI:1916456
KEYWORDS    STS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4522)
  AUTHORS   Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,
            Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,
            Leckie,M.P. and Green,E.D.
  TITLE     A collection of 1814 human chromosome 7-specific STSs
  JOURNAL   Genome Res. 7 (1), 59-64 (1997)
  MEDLINE   97189344
   PUBMED   9037602
REFERENCE   2  (bases 1 to 4522)
  AUTHORS   Green,E.D.
  TITLE     Human chromosome 7 STSs (1997)
  JOURNAL   Unpublished
COMMENT     Synonyms: OBS
            GDB: GDB:455256
            GDB_DSEG: OBS
            Contact: Eric D. Green
            Genome Technology Branch
            National Human Genome Research Institute/NIH
            49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
            Tel: 3014020201
            Fax: 3014024735
            Email: egreen@nhgri.nih.gov
            Primer A: CGTTAAGGGAAGGAACTCTGG
```

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          Primer B: TGGCTTAGAGGAGTCAGGGA
          STS size: 106
          PCR Profile:
                  Presoak:          0 degrees C for  0.00 minute(s)
                  Denaturation:    92 degrees C for  0.17 minute(s)
                  Annealing:       50 degrees C for  1.00 minute(s)
                  Polymerization:  72 degrees C for  1.00 minute(s)
                  PCR Cycles:      35
                  Thermal Cycler:  PerkinElmer 9600
          Protocol:
                  Template:        30-100 ng
                  Primer:          each 1 uM
                  dNTPs:           each 200 uM
                  Taq Polymerase:  0.05 units/ul
                  Total Vol:       10 ul

          Buffer:
                  MgCl2:           1.5 mM
                  KCl:             100 mM
                  Tris-HCl:        10 mM
                  NH4Cl:           5 mM
                  pH:              8.6

            This STS has been incorporated into the NHGRI chromosome 7
          physical map, but was developed by another investigator.   See
          GenBank record: D63710   For additional information about the NHGRI
          chromosome 7   mapping project, see
          http://www.nhgri.nih.gov/DIR/GTB/CHR7.   Also see Genomics
          11:548-64 (1991) [MUID=92128937].
FEATURES             Location/Qualifiers
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                     /clone_lib="Eric D. Green"
     gene            1. .4522
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     STS             423. .528
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     primer_bind     complement(509. .528)
BASE COUNT     1189 a   1032 c   1177 g   1124 t
ORIGIN


  Query Match           100.0%;  Score 239;  DB 11;  Length 4522;
  Best Local Similarity   100.0%;  Pred. No. 5e-62;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
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Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
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Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 TTTCTGAATAACATTTGTGTGGTGGGTTCTTTGGAAGGAGTGAGATCATTTTCTTATCT 1330


RESULT   7
AC018635
LOCUS       AC018635              163549 bp    DNA     linear   PRI 15-NOV-2001
DEFINITION  Homo sapiens chromosome 7 clone RP11-62J1, complete sequence.
ACCESSION   AC018635
VERSION     AC018635.7  GI:16930995
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 163549)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 163549)
  AUTHORS   Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-1999) Human Genome Center, University of
            Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 163549)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C.,
            Clendenning,J., Ivey,R.G. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   4  (bases 1 to 163549)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Nov 15, 2001 this sequence version replaced gi:13491250.
            -------------- Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: uwgchtgs@u.washington.edu
            -------------- Project Information
                Center project name: chr-7
                Center clone name: RP11-62J1 (djs169)
            ------------- Summary Statistics
                Assembly program: Phrap; version 0.990319
                Consensus quality: 163396 bases at least Q40
                Consensus quality: 163533 bases at least Q30
                Consensus quality: 163548 bases at least Q20
                Insert size: 177112; 11.9% error; agarose-fp
                Insert size: 163559; sum-of-contigs
                Quality coverage: 9.0x in Q20 bases; agarose-fp
                Quality coverage: 9.7x in Q20 bases; sum-of-contigs
            --------------
            Overlapping Sequences:
                5': RP11-339C9 (UWGC:djs166) AC018662 20141-bp clone overlap
                3': RP11-155G14 (UWGC:djs356) AC010655 54910-bp clone overlap
            --------------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible from the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double-stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., Phred
            quality >= 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            --------------------
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence-predicted fragments is given below.
             The electronically-digested sequence consists of both insert and
```

vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI		NsiI		BglII	
SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt
8696	8684	13216	13097	4728	4721
6	<800	3968	3969	2067	2031
2301	2289	4373	4368	15184	15086
198	<800	2295	2362	650	<800
3164	3163	439	<800	8876	8993
4222	4239	87	<800	2426	2447
7139	7181	154	<800	758	783
3111	3163	1047	1027	8355	8410
1017	1014	2497	2628	8468	8410
902	908	2616	2628	4250	4247
21	<800	2370	2509	3062	3085
7281	7181	338	<800	205	<800
4206	4239	2848	2904	3953	3970
4508	4496	7021	7007	1219	1240
8079	8107	205	<800	1246	1240
8552	8684	4535	4574	1394	1385
341	<800	2323	2362	5525	5461
77	<800	824	812	9907	9907
4415	4380	382	<800	1622	1595
3210	3163	8609	8741	13246	13175
589	<800	4206	4222	2221	2298
65	<800	17664	17766	1539	1513
10538	10720	1234	1208	2493	2447
5616	5536	7717	7723	1621	1595
1325	1320	420	<800	3410	3404
12632	13898	16266	16348	8455	8410
16469	16336	2956	2904	45	<800
5816	5688	1690	1682	2918	2896
606	<800	1757	1682	665	<800
2418	2394	319	<800	3671	3623
10242	10324	2735	2904	2218	2197
13881	13898	8193	8244	7262	7230
2012	1988	33175	33229	2329	2447
3481	3489	2284	2260	19523	19604
2711	2700	12824	12347	5408	5461
1719	1784			1161	1136
12014	12583			2573	2558
7	<800			5741	5807
				1494	1477
				1699	1717

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FEATURES             Location/Qualifiers
     source          1. .163549
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="7"
                     /clone="RP11-62J1"
                     /clone_lib="RPCI human BAC library 11"
     misc_feature    7183. .7191
                     /note="Single subclone region"
     STS             33185. .33290
                     /standard_name="sWSS2619"
     STS             46361. .46436
                     /standard_name="sWSS3617"
     misc_feature    57855. .58084
                     /note="Single subclone region"
     misc_feature    72400. .72469
                     /note="Single subclone region"
     misc_feature    73086. .73394
                     /note="Single subclone region"
     misc_feature    107287. .107288
                     /note="gi|154843|gb|J01829|TRN10IS13 and 9-bp target site
                     duplication excised from between bases 107287 and 108626
                     CTGATGAATCCCCTAATGATTTTGGTAAAAATCATTAAGTTAAGGTGGATACACATCT
                     TGTCATATGATCAAATGGTTTCGCGAAAAATCAATAATCAGACAACAAGATGTGCGAA
                     CTCGATATTTTACACGACTCTCTTTACCAATTCTGCCCCGAATTACACTTAAAACGAC
                     TCAACAGCTTAACGTTGGCTTGCCACGCATTACTTGACTGTAAAACTCTCACTCTTAC
                     CGAACTTGGCCGTAACCTGCCAACCAAAGCGAGAACAAAACATAACATCAAACGAATC
                     GACCGATTGTTAGGTAATCGTCACCTCCACAAAGAGCGACTCGCTGTATACCGTTGGC
                     ATGCTAGCTTTATCTGTTCGGGCAATACGATGCCCATTGTACTTGTTGACTGGTCTGA
                     TATTCGTGAGCAAAAACGACTTATGGTATTGCGAGCTTCAGTCGCACTACACGGTCGT
                     TCTGTTACTCTTTATGAGAAAGCGTTCCCGCTTTCAGAGCAATGTTCAAAGAAAGCTC
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  Query Match             100.0%;  Score 239;  DB 9;  Length 163549;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-62;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   33853 CTGGTTTCATTTCTACTGTGACTGATGTTACATCACAGTGTTTGCAATGGTGTTGCCCTG 33912

Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   33913 AGTGGATCTCCAAGGACCAGGTTATTTTAAAAAGATTTGTTTTGTCAAGTGTCATATGTA 33972

Qy     121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   33973 GGTGTCTGCACCCAGGGGTGGGGAATGTTTGGGCAGAAGGGAGAAGGATCTAGAATGTGT 34032

Qy     181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   34033 TTTCTGAATAACATTTGTGTGGTGGGTTCTTTGGAAGGAGTGAGATCATTTTCTTATCT 34091

RESULT   8
```

```
AB041360
LOCUS       AB041360               2935 bp    mRNA    linear   MAM 09-MAY-2000
DEFINITION  Felis catus ob mRNA for leptin, complete cds.
ACCESSION   AB041360
VERSION     AB041360.1  GI:7768655
KEYWORDS    leptin.
SOURCE      Felis catus white adipose tissue cDNA to mRNA.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 2935)
  AUTHORS   Sasaki,N., Iwase,M., Kimura,K., Ohishi,I. and Saito,M.
  TITLE     Molecular cloning of feline leptin cDNA
  JOURNAL   Published Only in DataBase (2000) In press
REFERENCE   2  (bases 1 to 2935)
  AUTHORS   Sasaki,N., Iwase,M., Kimura,K., Ohishi,I. and Saito,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-2000) Noriyasu Sasaki, Nippon Veterinary and
            Animal Science University, Division of Veterinary Biochemistry;
            Kyonancho 1-7-1, Musashino, Tokyo 180-8602, Japan
            (E-mail:noris@air.linkclub.or.jp, Tel:+81-422-31-4151,
            Fax:+81-422-31-7841)
FEATURES             Location/Qualifiers
     source          1. .2935
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /tissue_type="white adipose tissue"
     gene            30. .533
                     /gene="ob"
     CDS             30. .533
                     /gene="ob"
                     /codon_start=1
                     /product="leptin"
                     /protein_id="BAA95481.1"
                     /db_xref="GI:7768656"
                     /translation="MLCGPLCRFLWLWPYLSYVEAVPIRKVQDDTKTLIKTIVTRIND
                     ISHTQSVSSKQRVAGLDFIPGLHPVLSLSKMDQTLAIYQQILTGLPSRNVVQISNDLE
                     NLRDLLHLLASSKNCPLPRARGLETLESLGGALEASLYSTEVVALSRLQASLQDMLWR
                     LDLSPGC"
     polyA_signal    2914. .2919
BASE COUNT      703 a    718 c    804 g    710 t
ORIGIN
```

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  Query Match             57.7%;  Score 138;  DB 4;  Length 2935;
  Best Local Similarity   76.0%;  Pred. No. 2.4e-31;
  Matches  184;  Conservative    0;  Mismatches   55;  Indels    3;  Gaps    1;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           |||||||  |||||||  |||||||||||| | || ||||||||||||||||  ||||||||
Db    1118 CTGGTTTTGTTTCTACCGTGACTGATGTGAAATTACAGTGTTTGCAATGGCATTGCCCTG 1177

Qy      61 agtggatctccaaggaccaggttattttaaa---aagatttgttttgtcaagtgtcatat 117
           ||  ||||||||||||||||||  ||  |||   |||||   |||||||||||||| ||||
Db    1178 AGCAGATCTCCAAGGACCAGGTTCTTCCAAAAAGAAGATGAATTTTGTCAAGTGTGATAT 1237

Qy     118 gtaggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatg 177
           |||  |||  ||||||  | |||||||  |    |       |    | | | |    ||||||
Db    1238 ATAGATGTGTGCACCTGGAGGTGGGGGAACGTGTTAGTGGGAAGGGGAAGGATCAGAATG 1297

Qy     178 tgtttttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttat 237
           | ||||||||||  |||||||||||  ||||  ||||  |||  ||  |||   |||||||||  ||
Db    1298 TATTTTCTGAATTACATTTGTGTGATGGGCTCTTCGGATGGGGTGGAGTCATTTTCTCAT 1357

Qy     238 ct 239
           ||
Db    1358 CT 1359
```

```
RESULT   9
AF310264
LOCUS       AF310264               1076 bp    mRNA    linear   MAM 14-NOV-2000
DEFINITION  Ovis aries leptin mRNA, partial 3' UTR.
ACCESSION   AF310264
VERSION     AF310264.1  GI:11141758
KEYWORDS    .
SOURCE      sheep.
  ORGANISM  Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 1076)
  AUTHORS   Bonnet,M., Gourdou,I., Leroux,C., Chilliard,Y. and Djiane,J.
  TITLE     Leptin synthesis by ovine mammary gland: sequential involvement of
            adipose, epithelial and myoepithelial mammary cells during
            pregnancy and lactation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1076)
  AUTHORS   Bonnet,M., Gourdou,I., Leroux,C., Chilliard,Y. and Djiane,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-OCT-2000) ENA, INRA, URH-TALL, St. Genes Champanelle
            63122, France
FEATURES             Location/Qualifiers
     source          1. .1076
                     /organism="Ovis aries"
                     /db_xref="taxon:9940"
                     /tissue_type="mammary gland"
     3'UTR           <1. .>1076
                     /note="part of leptin gene"
BASE COUNT      262 a    235 c    305 g    274 t
ORIGIN
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  Query Match             56.2%;  Score 134.2;  DB 4;  Length 1076;
  Best Local Similarity   78.2%;  Pred. No. 3.8e-30;
  Matches  176;  Conservative    0;  Mismatches   43;  Indels    6;  Gaps    1;

Qy       6 ttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctgagtgg 65
           ||  |||||||||||||||  ||| || ||||||||||||||||  |||| |||| |||
Db       3 TTTGTTTCTACTGTGACTGACTTTAAATTACAGTGTTTGCAATGGCATTGCTCTGAATGG 62

Qy      66 atctccaaggaccaggttattttaaa------aagatttgttttgtcaagtgtcatatgt 119
           ||||| |||||||| ||||||||||      ||||    |||||||||||| |||| |
Db      63 ATCTCGAAGGACCAAGTTATTTTAAAAAGAAGAAGAAGAATTTTGTCAAGTGTAATATAT 122

Qy     120 aggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtg 179
           | ||  |  |||||| |||||| ||||| | |   |||||| |   |||| ||||||||
Db     123 TGCTGGGTATACCCAGAGGTGGGAAATGTGTTGATGGAAGGGGGGGAGATCCAGAATGTG 182

Qy     180 ttttctgaataacatttgtgtggtgggttctttggaaggagtgag 224
           |||||||||||||||| |||| ||| |||||||| || || ||
Db     183 TTTTCTGAATAACATTTTTGTGATGGACTCTTTGGATGGGGTAAG 227
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```
RESULT  10
AB020986
LOCUS       AB020986               2925 bp    mRNA    linear   MAM 28-NOV-2001
DEFINITION  Canis familiaris mRNA for leptin, complete cds.
ACCESSION   AB020986
VERSION     AB020986.1  GI:4038726
KEYWORDS    leptin.
SOURCE      Canis familiaris (isolate:1) adult male white adipose cDNA to mRNA,
            clone:inu-1.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (sites)
  AUTHORS   Iwase,M., Kimura,K., Sasaki,N., Komagome,R., Ishioka,K.,
            Morimatsu,M., Murakami,T. and Saito,M.
  TITLE     Canine leptin: cDNA cloning, expression and activity of recombinant
            protein
  JOURNAL   Res. Vet. Sci. 68 (2), 109-114 (2000)
  MEDLINE   20221602
REFERENCE   2  (bases 1 to 2925)
  AUTHORS   Iwase,M., Sasaki,N., Kazuhiro,K. and Saito,M.
  TITLE     Direct Submission
```

```
  JOURNAL   Submitted (10-DEC-1998) Miho Iwase, School of Veterinary Medicine,
            Hokkaido University, Laboratory of Biochemistry; N18, W9, Kita-ku,
            Sapporo, Hokkaido 060-0818, Japan
            (E-mail:v070003@vet.ec.hokudai.ac.jp, Tel:81-11-706-5206,
            Fax:81-11-757-0703)
COMMENT     On Dec 21, 1998 this sequence version replaced gi:4009339.
            Sequence updated (17-Dec-1998).
FEATURES             Location/Qualifiers
     source          1. .2925
                     /organism="Canis familiaris"
                     /isolate="1"
                     /db_xref="taxon:9615"
                     /clone="inu-1"
                     /sex="male"
                     /tissue_type="white adipose"
                     /dev_stage="adult"
     gene            32. .535
                     /gene="ob"
     CDS             32. .535
                     /gene="ob"
                     /note="49th amino acid (Gln) is deleted in some clone"
                     /codon_start=1
                     /product="leptin"
                     /protein_id="BAA35129.1"
                     /db_xref="GI:4009340"
                     /translation="MRCGPLCRFLWLWPYLSCVEAVPIRKVQDDTKTLIKTIVARIND
                     ISHTQSVSSKQRVAGLDFIPGLQPVLSLSRMDQTLAIYQQILNSLHSRNVVQISNDLE
                     NLRDLLHLLASSKSCPLPRARGLETFESLGGVLEASLYSTEVVALNRLQAALQDMLRR
                     LDLSPGC"
     polyA_signal    2875. .2880
BASE COUNT      742 a    707 c    766 g    710 t
ORIGIN
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  Query Match             54.4%;  Score 130;  DB 4;  Length 2925;
  Best Local Similarity   78.7%;  Pred. No. 6.5e-29;
  Matches  181;  Conservative    0;  Mismatches   45;  Indels    4;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||  |   |||||||||||||| |||||||  || ||||||||||||||||  ||||||||
Db    1123 CTGGCTATGTTTCTACTGTGACGGATGTTAAATTACAGTGTTTGCAATGGCATTGCCCTG 1182

Qy      61 agtggatctccaaggaccaggttatttttaaa---aagatttgttttgtcaagtgtcatat 117
           || ||||||||||||||||||||||||| |||   |||||   |||||||| |||| ||||
Db    1183 AGCGGATCTCCAAGGACCAGGTTATTTCAAAAAGAAGATGAATTTTGTCATGTGTGATAT 1242

Qy     118 gtaggtgtctgcacccaggggt-ggggaatgtttgggcagaagggagaaggatctagaat 176
           ||| ||| || |||  | ||| || ||| || |  |||| | || ||||||||  || ||
Db    1243 ATAGATGTGTGTACCTGGAGGTAGGAGAACGTGTTAGCAGGAAGGGGAAGGATCCAGGAT 1302

Qy     177 gtgttttctgaataacatttgtgtggtgggttctttggaaggagtgagat 226
           || |||| ||||| |||||||| | |||| |||| | | |||| | | |
Db    1303 GTATTTTTTGAATTACATTTGTGCGATGGGCTCTTCGAATGGAGGGGGGT 1352
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```
RESULT  11
E59801
LOCUS       E59801                  2925 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Canine obsity gene, its gene product and process for producing it,
            and assaying regaent and assay.
ACCESSION   E59801
VERSION     E59801.1  GI:18622637
KEYWORDS    JP 2000279171-A/18.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 2925)
  AUTHORS   Honsho,T. and Saito,M.
  TITLE     Canine obsity gene, its gene product and process for producing it,
            and assaying regaent and assay
  JOURNAL   Patent: JP 2000279171-A 18 10-OCT-2000;
            MORINAGA & CO LTD
COMMENT     OS   Canis sp. (dog)
            PN   JP 2000279171-A/18
            PD   10-OCT-2000
            PF   30-MAR-1999 JP 1999088295
            PR
            PI   TSUTOMU HONSHO,MASAYUKI SAITO
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/21,C12P21/02,G01N33/53//
            PC   (C12P21/02,C12R1:19),C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .2894
            FT                   /organism='Canis sp. (dog)'.
FEATURES             Location/Qualifiers
     source          1. .2925
                     /organism="Canis sp."
                     /db_xref="taxon:9616"
BASE COUNT      742 a    707 c    766 g    710 t
ORIGIN
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  Query Match             54.4%;  Score 130;  DB 6;  Length 2925;
  Best Local Similarity   78.7%;  Pred. No. 6.5e-29;
  Matches  181;  Conservative    0;  Mismatches   45;  Indels    4;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           ||||  |   |||||||||||||| |||||||  || ||||||||||||||||  ||||||||
Db    1123 CTGGCTATGTTTCTACTGTGACGGATGTTAAATTACAGTGTTTGCAATGGCATTGCCCTG 1182

Qy      61 agtggatctccaaggaccaggttatttttaaa---aagatttgttttgtcaagtgtcatat 117
           || ||||||||||||||||||||||||| |||   |||||   |||||||| |||| ||||
Db    1183 AGCGGATCTCCAAGGACCAGGTTATTTCAAAAAGAAGATGAATTTTGTCATGTGTGATAT 1242

Qy     118 gtaggtgtctgcacccaggggt-ggggaatgtttgggcagaagggagaaggatctagaat 176
           ||| ||| || |||  | ||| || ||| || |  |||| | || ||||||||  || ||
Db    1243 ATAGATGTGTGTACCTGGAGGTAGGAGAACGTGTTAGCAGGAAGGGGAAGGATCCAGGAT 1302

Qy     177 gtgttttctgaataacatttgtgtggtgggttctttggaaggagtgagat 226
           || |||| ||||| |||||||| | |||| |||| | | |||| | | |
Db    1303 GTATTTTTTGAATTACATTTGTGCGATGGGCTCTTCGAATGGAGGGGGGT 1352
```

```
RESULT  12
AR175617
LOCUS       AR175617                2793 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 1 from patent US 6309853.
ACCESSION   AR175617
VERSION     AR175617.1  GI:17916916
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2793)
  AUTHORS   Friedman,J.M., Zhang,Y. and Proenca,R.
  TITLE     Modulators of body weight, corresponding nucleic acids and
            proteins, and diagnostic and therapeutic uses thereof
  JOURNAL   Patent: US 6309853-A 1 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .2793
                     /organism="unknown"
BASE COUNT      689 a    653 c    740 g    711 t
ORIGIN
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  Query Match             33.7%;  Score 80.6;  DB 6;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 6.6e-14;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy       1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
           |||||||  ||||||  |||||||||   ||    |   |||||||  ||  |||||
Db    1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy      61 agtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgta 120
           ||| |       |     ||||   ||  ||||   |||||||||||||| |||||||
```

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Db   1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT  13
AX088104
LOCUS       AX088104               2793 bp    DNA     linear   PAT 17-MAR-2001
DEFINITION  Sequence 1 from Patent WO0113935.
ACCESSION   AX088104
VERSION     AX088104.1  GI:13397026
KEYWORDS    .
SOURCE      Murinae gen. sp.
  ORGANISM  Murinae gen. sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE   1  (bases 1 to 2793)
  AUTHORS   Banks,W.A.
  TITLE     Modulation of the blood-brain barrier transporter for leptin
  JOURNAL   Patent: WO 0113935-A 1 01-MAR-2001;
            Tulane University (US)
FEATURES             Location/Qualifiers
     source          1. .2793
                     /organism="Murinae gen. sp."
                     /db_xref="taxon:39108"
                     /note="Murine ob (leptin) cDNA"
     sig_peptide     57. .59
     CDS             57. .560
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC34684.1"
                     /db_xref="GI:13397027"
                     /translation="MCWRPLCRFLWLWSYLSYVQAVPIQKVQDDTKTLIKTIVTRIND
                     ISHTQSVSAKQRVTGLDFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLE
                     NLRDLLHLLAFSKSCSLPQTSGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQ
                     LDVSPEC"
     mat_peptide     60. .557
                     /product="unnamed"
BASE COUNT      689 a    653 c    740 g    711 t
ORIGIN


  Query Match             33.7%;  Score 80.6;  DB 6;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 6.6e-14;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
          |||||||  ||||||  |||||||||   ||    |   |||||||  ||  |||||
Db   1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy     61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
            ||| |       |    ||||   ||  ||||   |||||||||||||| |||||||
Db   1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT  14
MMU18812
LOCUS       MMU18812               2793 bp    mRNA    linear   ROD 30-MAR-1995
DEFINITION  Mus musculus obese precursor (ob) mRNA, complete cds.
ACCESSION   U18812
VERSION     U18812.1  GI:746416
KEYWORDS    .
SOURCE      mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2793)
  AUTHORS   Zhang,Y., Proenca,R., Maffei,M., Barone,M., Leopold,L. and
            Friedman,J.M.
  TITLE     Positional cloning of the mouse obese gene and its human homologue
  JOURNAL   Nature 372 (6505), 425-432 (1994)
  MEDLINE   95075453
REFERENCE   2  (bases 1 to 2793)
  AUTHORS   Friedman,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-1994) Jeffrey M. Friedman, Howard Hughes Medical
            Institute, The Rockefeller University, P.O. Box 305, 1230 York
            Ave., New York, NY 10021, USA
COMMENT     On Mar 30, 1995 this sequence version replaced gi:603287.
FEATURES             Location/Qualifiers
     source          1. .2793
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="6"
                     /map="15.7 cM"
     gene            1. .2793
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     CDS             57. .560
                     /gene="ob"
                     /standard_name="obese precursor"
                     /codon_start=1
                     /protein_id="AAA64564.1"
                     /db_xref="GI:603288"
                     /translation="MCWRPLCRFLWLWSYLSYVQAVPIQKVQDDTKTLIKTIVTRIND
                     ISHTQSVSAKQRVTGLDFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLE
                     NLRDLLHLLAFSKSCSLPQTSGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQ
                     LDVSPEC"
     sig_peptide     57. .119
                     /gene="ob"
                     /note="putative"
     mat_peptide     120. .557
                     /gene="ob"
                     /standard_name="obese"
                     /product="unnamed"
BASE COUNT      689 a    653 c    740 g    711 t
ORIGIN


  Query Match             33.7%;  Score 80.6;  DB 10;  Length 2793;
  Best Local Similarity   65.4%;  Pred. No. 6.6e-14;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
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Db   1225 CTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAACACGTTTGCAGCGGCATTGCC--- 1281

Qy     61 agtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgta 120
            ||| |       |    ||||   ||  ||||   |||||||||||||| |||||||
Db   1282 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 1339

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
          | | ||||||   |||| | | |||| |  |  | |||| ||||||||  ||| ||||
Db   1340 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 1398

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db   1399 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 1449


RESULT  15
AC072048/c
LOCUS       AC072048               214257 bp    DNA     linear   HTG 15-NOV-2001
```

```
DEFINITION  Mus musculus chromosome 6 clone RP23-189E15 strain C57BL6/J,
            WORKING DRAFT SEQUENCE, 14 unordered pieces.
ACCESSION   AC072048
VERSION     AC072048.2  GI:16930942
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 214257)
  AUTHORS   Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q.,
            Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian,S.D.,
            McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y.,
            Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Zhang,L.-H. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214257)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUN-2000) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     On Nov 15, 2001 this sequence version replaced gi:8313202.
            -------------- Genome Center
                 Center: NIH Intramural Sequencing Center
                 Center code: NISC
                 Web site: http://www.nisc.nih.gov
                 Contact: nisc_mouse@nhgri.nih.gov
            -------------- Project Information
                 Center project name: wp
                 Center clone name: 189E15
            -------------- Summary Statistics
                 Sequencing vector: plasmid; n/a; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990319
                 Consensus quality: 206853 bases at least Q40
                 Consensus quality: 207842 bases at least Q30
                 Consensus quality: 208446 bases at least Q20
                 Insert size: 209000; agarose-fp
                 Insert size: 197000; pulse-field-gel
                 Insert size: 212957; sum-of-contigs
                 Quality coverage: 11.38x in Q20 bases; agarose-fp
                 Quality coverage: 12.07x in Q20 bases; pulse-field-gel
                 Quality coverage: 11.17x in Q20 bases; sum-of-contigs
            --------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 14 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     6798: contig of 6798 bp in length
            *     6799     6898: gap of unknown length
            *     6899    15014: contig of 8116 bp in length
            *    15015    15114: gap of unknown length
            *    15115    24240: contig of 9126 bp in length
            *    24241    24340: gap of unknown length
            *    24341    32924: contig of 8584 bp in length
            *    32925    33024: gap of unknown length
            *    33025    44801: contig of 11777 bp in length
            *    44802    44901: gap of unknown length
            *    44902    55618: contig of 10717 bp in length
            *    55619    55718: gap of unknown length
            *    55719    69004: contig of 13286 bp in length
            *    69005    69104: gap of unknown length
            *    69105    82272: contig of 13168 bp in length
            *    82273    82372: gap of unknown length
            *    82373    99277: contig of 16905 bp in length
            *    99278    99377: gap of unknown length
            *    99378   113883: contig of 14506 bp in length
            *   113884   113983: gap of unknown length
            *   113984   133941: contig of 19958 bp in length
            *   133942   134041: gap of unknown length
            *   134042   149119: contig of 15078 bp in length
            *   149120   149219: gap of unknown length
            *   149220   175493: contig of 26274 bp in length
            *   175494   175593: gap of unknown length
            *   175594   214257: contig of 38664 bp in length.
FEATURES             Location/Qualifiers
     source          1. .214257
                     /organism="Mus musculus"
                     /strain="C57BL6/J"
                     /db_xref="taxon:10090"
                     /chromosome="6"
                     /clone="RP23-189E15"
                     /clone_lib="RPCI mouse BAC library 23"
     misc_feature    1. .6798
                     /note="assembly_fragment"
     misc_feature    6899. .15014
                     /note="assembly_fragment"
     misc_feature    15115. .24240
                     /note="assembly_fragment"
     misc_feature    24341. .32924
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     misc_feature    33025. .44801
                     /note="assembly_fragment"
     misc_feature    44902. .55618
                     /note="assembly_fragment"
     misc_feature    55719. .69004
                     /note="assembly_fragment"
     misc_feature    69105. .82272
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     misc_feature    82373. .99277
                     /note="assembly_fragment"
     misc_feature    99378. .113883
                     /note="assembly_fragment"
     misc_feature    113984. .133941
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     misc_feature    149220. .175493
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     misc_feature    175594. .214257
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:left"
BASE COUNT    55999 a  50290 c  50579 g  56076 t   1313 others
ORIGIN


  Query Match            33.7%;  Score 80.6;  DB 2;  Length 214257;
  Best Local Similarity  65.4%;  Pred. No. 4.6e-14;
  Matches  151;  Conservative    0;  Mismatches   74;  Indels    6;  Gaps    2;

Qy      1 ctggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctg 60
          ||||||| |||||| |||||||||    ||   | | |||||||  ||  |||||
Db 183716 CTGGTTTTGTTTCTATTGTGACTGACTCTATGCAAACACGTTTGCAGCGGCATTGCC--- 183658

Qy     61 agtggatctccaaggaccaggttatttaaaaagatttgttttgtcaagtgtcatatgta 120
           ||| |      |    ||||   ||  ||||   ||||||||||||| |||||||
Db 183659 --GGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTTTGTCAAGTGTAATATGTA 183602

Qy    121 ggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgt 180
            | | ||||||   |||| | | |||| |   |  | |||| ||||||||  ||| ||||
Db 183601 TCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGTGAAGGATCCGGAA-GTGT 183543

Qy    181 tttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattt 231
          | ||||||| |||| |||||||| || | ||  ||| | |||||    |||
Db 183542 TCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGAGGCATTTT 183492
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Search completed: June 13, 2002, 15:50:57
Job time: 10869 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 13, 2002, 12:49:43 ; Search time 1785.18 Seconds
(without alignments)
1806.973 Million cell updates/sec

Title: US-09-437-458-17
Perfect score: 239
Sequence: 1 ctggtttcatttctactgtg.....gtgagatcattttcttatct 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	40.4	16.9	465	12	AQ004645	AQ004645 CIT-HSP-2
c	2	39.2	16.4	1050	12	CNS013NS	AL103090 Drosophil
	3	39.2	16.4	1101	12	CNS00LT2	AL078714 Drosophil
	4	38.4	16.1	1201	12	CNS016BY	AL106552 Drosophil
	5	36.4	15.2	884	12	CNS006U0	AL065923 Drosophil
	6	36.4	15.2	1201	12	CNS0162X	AL106227 Drosophil
	7	36.2	15.1	541	10	BE322138	BE322138 NF010E03I
c	8	35.6	14.9	621	10	BM121183	BM121183 L0949E03-
c	9	35.6	14.9	848	12	CNS00GWQ	AL072642 Drosophil
	10	35.6	14.9	1101	12	CNS000D1	AL065414 Drosophil
	11	35.6	14.9	1101	12	CNS00Z7O	AL097326 Drosophil
c	12	35.4	14.8	376	12	AQ260214	AQ260214 CITBI-E1-
	13	35.4	14.8	637	12	AZ589172	AZ589172 1M0398A06
c	14	35.2	14.7	897	12	CNS015FK	AL105386 Drosophil
c	15	34.8	14.6	859	12	CNS004YY	AL055406 Drosophil
c	16	34.6	14.5	791	10	BG474557	BG474557 602517334
	17	34.4	14.4	621	12	AZ235467	AZ235467 RPCI-23-6
c	18	34.4	14.4	1101	12	CNS016JY	AL106840 Drosophil
c	19	34.2	14.3	939	12	CNS00CNG	AL059400 Drosophil
c	20	34.2	14.3	1101	12	CNS0039G	AL063921 Drosophil
	21	34	14.2	436	10	BF408218	BF408218 UI-R-BJ2-
	22	34	14.2	633	10	BM390047	BM390047 UI-R-CN1-
c	23	33.8	14.1	316	9	BB490430	BB490430 BB490430
	24	33.8	14.1	328	9	AA668450	AA668450 ab85g05.s
	25	33.8	14.1	328	9	AA668464	AA668464 ab86a05.s
	26	33.8	14.1	522	10	BM343932	BM343932 rr44g03.y
c	27	33.8	14.1	877	12	AQ867363	AQ867363 nbeb0031O
c	28	33.8	14.1	882	12	AZ686073	AZ686073 ENTME14TR
	29	33.8	14.1	895	12	CNS0071A	AL066286 Drosophil
c	30	33.8	14.1	904	12	AZ550922	AZ550922 ENTFL90TR
c	31	33.8	14.1	1127	12	CNS01XWK	AL172253 Tetraodon
c	32	33.6	14.1	500	9	AU086071	AU086071 AU086071
	33	33.6	14.1	712	12	AZ382973	AZ382973 1M0140P03
	34	33.4	14.0	411	10	BG304410	BG304410 f186h02.y
c	35	33.4	14.0	453	9	AU006663	AU006663 AU006663
	36	33.4	14.0	743	12	CNS0406F	AL268512 Tetraodon
c	37	33.4	14.0	793	12	CNS043S0	AL273177 Tetraodon
	38	33.4	14.0	924	10	BG336429	BG336429 602405370
c	39	33.2	13.9	318	9	AV163550	AV163550 AV163550
	40	33.2	13.9	693	9	BB358710	BB358710 BB358710
c	41	33.2	13.9	840	12	BH165678	BH165678 ENTTS02TF
	42	33.2	13.9	859	12	CNS00KLL	AL077728 Drosophil
	43	33.2	13.9	924	12	BH150220	BH150220 ENTPL95TR
c	44	33.2	13.9	967	12	CNS00KTZ	AL078030 Drosophil
	45	33.2	13.9	1003	12	AG076031	AG076031 Pan trogl

ALIGNMENTS

RESULT 1
AQ004645/c
LOCUS AQ004645 465 bp DNA linear GSS 26-JUN-1998
DEFINITION CIT-HSP-2127C7.TF CIT-HSP Homo sapiens genomic clone 2127C7, DNA sequence.
ACCESSION AQ004645
VERSION AQ004645.1 GI:3081100
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 465)
AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Kim,U.-J., Shizuya,H., Simon,M. and Venter,J.C.
TITLE Use of a human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
FEATURES Location/Qualifiers
source 1..465
/organism="Homo sapiens"
/db_xref="GDB:7086018"
/db_xref="taxon:9606"
/clone="2127C7"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"

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                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII"
BASE COUNT       129 a    125 c     69 g    142 t
ORIGIN


  Query Match             16.9%;  Score 40.4;  DB 12;  Length 465;
  Best Local Similarity   51.1%;  Pred. No. 0.61;
  Matches   95;  Conservative    0;  Mismatches   91;  Indels    0;  Gaps    0;

Qy      47 atggtgttgccctgagtggatctccaaggaccaggttattttaaaaagatttgttttgtc 106
           | || |  ||| |||  | | | |    ||  |||  |||  | |||   |  || |||
Db     437 AAGGAGGAGCCTTGATGGTAGCACAGCAGAAAAGGAAATTAGAGAAAAGCTGCTTCTGTT 378

Qy     107 aagtgtcatatgtaggtgtctgcacccaggggtggggaatgtttgggcagaagggagaag 166
             ||||    | ||  | ||| | ||   |  | ||| | |  |  |   |    | | |
Db     377 GGGTGTGCCTTATAAATCTCTACTCCACTGTTTTGGGGAAGCATCAGTCAATTACACATG 318

Qy     167 gatctagaatgtgttttctgaataacatttgtgtggtgggttctttggaaggagtgagat 226
           | ||  ||||   |||  ||   |    ||||  | |||   |   |||||  ||||||
       317 GCTCGTGAATACTTTTGGTGTTCATGGATTGTTCTGGGGGACTTGAAGAAGGGTTGAGAT 258

Qy     227 catttt 232
           |  | |
Db     257 CTATAT 252


RESULT   2
CNS013NS/c
LOCUS       CNS013NS                1050 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN10C02 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL103090
VERSION     AL103090.1  GI:5614701
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1050)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1050
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN10C02"
                     /note="end : SP6"
BASE COUNT       308 a    203 c     14 g    328 t    197 others
ORIGIN


  Query Match             16.4%;  Score 39.2;  DB 12;  Length 1050;
  Best Local Similarity   36.5%;  Pred. No. 1.5;
  Matches   65;  Conservative   36;  Mismatches   77;  Indels    0;  Gaps    0;

Qy      60 gagtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgt 119
             | |:|||  :  :| :   : :  ||||:  | |:  |:::|  || |:  :|  |
Db     644 GGGKGGAGGKTKRATKGAGTKTKAGGTTTAWTTGGGTKGTTKKKGGAAAATKAATKAATT 585

Qy     120 aggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtg 179
             | |      :   | ::| |||:  :|  : ::  |  ||| | :|||  :||  :|||
Db     584 TGATCMGSMGMAGWAAKKGAGGGSKGKGGAKTBKAKGKGGGGGGGRGGAGKDAGTKKGTG 525

Qy     180 ttttctgaataacatttgtgtggtgggttctttggaaggagtgagatcatttttcttat 237
                 ||| : |:||:::|| :| |   :|| | |:||:  | :| |||:| ||:|
Db     524 GAAARMAAATGMAAWTTKWKTGTKGCGCAAWTTTGGADGARAAATWTWATTWTTTTWT 467


RESULT   3
CNS00LT2
LOCUS       CNS00LT2                1101 bp    DNA     linear   GSS 14-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL078714
VERSION     AL078714.1  GI:5102004
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR48P19"
                     /note="end : TET3"
BASE COUNT       469 a      6 c     69 g    151 t    406 others
ORIGIN


  Query Match             16.4%;  Score 39.2;  DB 12;  Length 1101;
  Best Local Similarity   22.3%;  Pred. No. 1.5;
  Matches   49;  Conservative   82;  Mismatches   89;  Indels    0;  Gaps    0;

Qy       5 tttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctgagtg 64
           |||  ||| :  | |   |  | ||| || | |   |||: :|   : ||:   ::|
Db     651 TTTTTTTTAKTKTTTTTTTTTTATTAAATAAAAAAWTTTDTWAAAWWTTTKKKKKKAAAA 710

Qy      65 gatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgtaggtg 124
           : : :   ::||  | :|: ::::||:|| :::::::  ::   |::     ::: ::::
Db     711 DKWKDAKKWDGAKKATKTKKKDKKAAWAAADKKDRKKGGKKKGKGKKGKKGGKKKKKKKK 770

Qy     125 tctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgttttc 184
             |      :: |::: :: |::::::      ::: |  :: :   :    ::|::|
Db     771 GKGGWGKKGKKKAGDDDAKDKTKKKKKKAATTTTKKKKGKKKKKKAAKKKKAADRTKKTK 830
```

```
Qy    185 tgaataacatttgtgtggtgggttctttggaaggagtgag 224
          ::|| || | :: :::|:::::|: :|||::  :: ::: |
Db    831 WDAAAAAAAAKKTKDKGKKKKKTKKKTTKKKKKKKKKKGG 870


RESULT   4
CNS016BY
LOCUS       CNS016BY               1201 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN15C08 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106552
VERSION     AL106552.1  GI:5622489
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
  FERENCE   1  (bases 1 to 1201)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN15C08"
                     /note="end : SP6"
BASE COUNT      344 a    106 c    179 g    353 t    219 others
ORIGIN


  Query Match            16.1%;  Score 38.4;  DB 12;  Length 1201;
  Best Local Similarity  36.1%;  Pred. No. 2.5;
  Matches   52;  Conservative   36;  Mismatches   56;  Indels    0;  Gaps    0;

Qy     82 ttattttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtgg 141
          || ||::|||| ::|| ||:| :   | :   | ::: ||| | |  :   :::  :||
Db    920 TTTTTWWAAAAAARWTTTTTWTTKKKKGGRATTTTKKKGGGTTTKTAADGGGRRKTTKGG 979

Qy    142 ggaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtgtg 201
          |:|:  |||::|   || ::||     : : :|| :| |||| ::   | | |::: |
Db    980 GRARATTTTKKGWTAAAARRAGTTTTTKKDKRAAARTTTTTTGGRDGAKARAATKKKTTT 1039

Qy    202 gtgggttctttggaaggagtgaga 225
          |||  :|   ||:  :: :: | |
Db   1040 GTGTAKTGGGTGKKKRKGKDAAAA 1063


RESULT   5
CNS006U0
LOCUS       CNS006U0               884 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14N21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065923
VERSION     AL065923.1  GI:4944891
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .884
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR14N21"
                     /note="end : T7"
BASE COUNT      230 a     62 c    139 g    124 t    329 others
ORIGIN


  Query Match            15.2%;  Score 36.4;  DB 12;  Length 884;
  Best Local Similarity  13.1%;  Pred. No. 8.6;
  Matches   26;  Conservative   95;  Mismatches   77;  Indels    0;  Gaps    0;

Qy     38 gtgtttgcaatggtgttgccctgagtggatctccaaggaccaggttatttttaaaaagatt 97
          | |:::|   |||:: ||   :  :::: : :    :|    :::  |:::     : |
Db    658 GGGKKKGGTKTGGKDGTGGKKKTTKKKKKKKKGTKGKGKGKTKKKSGTKKKKGGTGKGTG 717

Qy     98 tgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtggggaatgtttgggcaga 157
          |: | |::   |:|:  : :|  |::|: ::      :::::|::: ||::|:|:  |
Db    718 TKGTGTKKKKGGKGKGGKKKGGKGKKGKKKKKGKKKKKKKKKGKKKKKTGKKTKGKKGGT 777

Qy    158 agggagaaggatctagaatgtgttttctgaataacatttgtgtggtgggttctttggaag 217
          ::| :  :: : : :  ::::::::: ::  :    :::::::::: :::: :::::  :
Db    778 KKKGKKKGKKTKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKTKKKKKKKKKKCK 837

Qy    218 gagtgagatcattttctt 235
          : ::: : :  :::: ::
Db    838 KKKKKKKKKKKKKKKKK 855


RESULT   6
CNS0162X
LOCUS       CNS0162X               1201 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN15O19 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106227
VERSION     AL106227.1  GI:5620779
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
```

```
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN15O19"
                     /note="end : T7"
BASE COUNT       360 a    103 c    276 g    188 t    274 others
ORIGIN


  Query Match           15.2%;  Score 36.4;  DB 12;  Length 1201;
  Best Local Similarity   30.3%;  Pred. No. 9.1;
  Matches   71;  Conservative   64;  Mismatches   98;  Indels    1;  Gaps    1;

Qy       2 tggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctga 61
           | ::::  ||:    |:|   |: | :|| |:     |  :|:       |:|    ||
Db     695 TTDWWKTTTTDTATGTDTTTTKTTAKTAAAWWGWTWTTADTDTGTGTTAGWTTDWTTGT 754

Qy      62 gtggatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgtag 121
           ||| || |  :  ||   ::| | ||: | ::::|  | |:     || :: :|::|::
Db     755 GTGTATATATRGTGATATKRTGARTTKTATWWKWTGAGATKRTARGAGAKK-WTRWGWRA 813

Qy     122 gtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgtt 181
           ||||    |   |: :|:|:::  ||::| |:  ::|: | |   :|: :::::||::|:
Db     814 GTGTARAGAWRWAKARGKGKKKKKTGKKTWGKDKRWAKWGTGTGAKAWTWRRDATRWGWG 873

Qy     182 ttctgaataacatttgtgtggtgggttctttggaaggagtgagatcatttttctt 235
           :| | |  :| |:|    : || : ::   : :|:: || |:: |  |:|  :|
Db     874 WTATTATAWATAWTAWRWKTGTAKTDWTAAKAKAWRAAGAGRKTTTKTKTRDDT 927


RESULT   7
BE322138
LOCUS       BE322138                541 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  NF010E03IN1F1020 Insect herbivory Medicago truncatula cDNA clone
            NF010E03IN 5', mRNA sequence.
  ACCESSION   BE322138
  VERSION     BE322138.2  GI:11964127
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 541)
  AUTHORS   Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
            ,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula insect herbivory library
  JOURNAL   Unpublished (2000)
COMMENT     On Jul 14, 2000 this sequence version replaced gi:9195915.
            Contact: Korth K
            Dept. of Plant Pathology
            University of Arkansas
            217 Plant Science Building, Fayetteville, AR 72701, USA
            Tel: 501 575 5191
            Fax: 501 575 7601
            Email: kkorth@comp.uark.edu
            Medicago Genome Initiative accession: MGI:S:23963
            Insert Length: 685   Std Error: 0.00
            Plate: 010  row: E  column: 03
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .541
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF010E03IN"
                     /clone_lib="Insect herbivory"
                     /tissue_type="local and systemic leaves"
                     /dev_stage="mature"
                     /note="Vector: Lambda Zap; Library was produced from fully
                     expanded M. truncatula leaves of plants fed upon by
                     Spodoptera exigua (beet armyworm) for 24 hours. Systemic
                     (undamaged leaves from injured plants) and wounded leaves
                     were harvested and pooled."
BASE COUNT       183 a    106 c    100 g    152 t
ORIGIN


  Query Match           15.1%;  Score 36.2;  DB 10;  Length 541;
  Best Local Similarity   54.0%;  Pred. No. 9.1;
  Matches   74;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy      96 tttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtggggaatgtttgggca 155
           |||||  ||  |  |||   | || |    ||   |     ||| |  || | |  ||
Db     384 TTTGTGATGGAATATGTACGAGGTGGTGAGCTTTTCAACAAGGTTGCTAAAGGTAAGGTT 443

Qy     156 gaagggagaaggatctagaatgtgttttctgaataacatttgtgtggtgggttctttgga 215
           ||| | ||||    | || |  | ||||| | |    || ||||  || || | ||||
Db     444 GAAAGAAGAAGTTGCAAGGAAATATTTTCAGCAGTTAATATGTGCTGTTGGATTTTTGTC 503

Qy     216 aggagtgagatcatttt 232
           | |   ||| |  ||||
Db     504 ATGCTAGAGGTGTTTTT 520


RESULT   8
BM121183/c
LOCUS       BM121183                621 bp    mRNA    linear   EST 01-FEB-2002
DEFINITION  L0949E03-3 NIA Mouse Newborn Kidney cDNA Library (Long) Mus
            musculus cDNA clone L0949E03 3', mRNA sequence.
ACCESSION   BM121183
VERSION     BM121183.1  GI:17089209
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Pantano,S., Lim,M.K.
            and Ko,M.S.H.
  TITLE     Systematic Analyses of NIA Mouse Newborn Kidney cDNA Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: L0949  row: E  column: 03
            Seq primer: -21M13 Forward
            High quality sequence stop: 621
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="niaEST:L0949E03-3"
                     /db_xref="taxon:10090"
                     /clone="L0949E03"
                     /clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long)"
                     /tissue_type="Newborn Kidney"
                     /dev_stage="Newborn"
```

/lab_host="DH10B"
/note="Organ: kidney; Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11:1553-1558 (2001). [PMID:11544199]). In brief ,double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from 26 microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes, and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao (NIA)."
BASE COUNT 172 a 136 c 129 g 184 t
ORIGIN

Query Match 14.9%; Score 35.6; DB 10; Length 621;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
Qy    134 aggggtggggaatgtttgggcagaagggagaaggatctagaatgtgttttctgaataaca 193
          |||   ||| |||||||  ||||||  ||  |  |  |  ||||  | ||  ||| |
Db    578 AGGCAAGGGCAATGTTTTGGCAGACAGGGAATAGTACAGGAATCAGATTCATGACTGCAG 519

Qy    194 tttgtgtggtgggttctttggaaggagtgagatcattt 231
          | |||    || || || ||||| |||  | ||  |||
Db    518 TCTGTACCTTGAGTGCTCTGGAAAGAGCCATATTGTTT 481
```

RESULT 9
CNS00GWQ/c
LOCUS CNS00GWQ 848 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR34B02 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL072642
VERSION AL072642.1 GI:4952523
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 848)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .848
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR34B02"
/note="end : TET3"
BASE COUNT 87 a 120 c 35 g 259 t 347 others
ORIGIN

Query Match 14.9%; Score 35.6; DB 12; Length 848;
Best Local Similarity 21.4%; Pred. No. 14;
Matches 47; Conservative 81; Mismatches 92; Indels 0; Gaps 0;

```
Qy      2 tggtttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctga 61
          :|:| | |: |:| ::: :  |  | ||   |    :|:|  :|  :|:: : :   |:
Db    794 KGKTGTKAKGTBTGHKKNKTKTTTTTTTNTTTTSTYBTKTGGKCBKKGBKTKNBWGKTKT 735

Qy     62 gtggatctccaaggaccaggttattttaaaaagatttgttttgtcaagtgtcatatgtag 121
          :|:: : : :     :  : :|:::|:     : :: : ::: |   :::   :  : :|
Db    734 KTKKTKKDNBTKTTKBTKKTKTDKKTKTKTKKKTKYSBGKKBTTGKKKKKGKTKKKGKGDG 675

Qy    122 gtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgtt 181
          |:: ::::     ||::  |||  : : :::| :|  ::: ||:|| | | :  |:::|
Db    674 GKKGVKKSGGGGGGGKKGTGGGGGKCKGKKKGKDGKGKKKGGARGGTTTTTKTKTKKKTA 615

Qy    182 ttctgaataacatttgtgtggtgggttctttggaaggagt 221
          ::   ||    ||:|::::| :: ||   ::: |:: :|:
Db    614 WDWAAAAAKKKATDTKKKKGTKRAGTGGRKDRAARKADGK 575
```

RESULT 10
CNS000D1
LOCUS CNS000D1 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR01J16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL065414
VERSION AL065414.1 GI:4938827
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"

```
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR01J16"
                     /note="end : TET3"
BASE COUNT      280 a    104 c    123 g    211 t    383 others
ORIGIN


  Query Match             14.9%;  Score 35.6;  DB 12;  Length 1101;
  Best Local Similarity   14.1%;  Pred. No. 15;
  Matches   31;  Conservative  111;  Mismatches   78;  Indels    0;  Gaps    0;

Qy       5 tttcatttctactgtgactgatgttacatcacagtgtttgcaatggtgttgccctgagtg 64
           ||: | |: :   :::|  ||::::: :  :  ::|:: :    :|::::    :: |::
Db     732 TTKRAATDKWKWRKKKATAGAWDWDDARRGRGGRWGDKRRRTGARGDKDKTGKKKKTGDK 791

Qy      65 gatctccaaggaccaggttatttttaaaaagatttgttttgtcaagtgtcatatgtaggtg 124
           :::     ::|:  ||| ::: : :|::|:::|::|   :: |::::  :::: : ::|
Db     792 RDKGGGDGDRGDGGAGGGDRDRDARARRARWDTKDTRGAKDKADKKKAGRKRKWWTRKTW 851

       125 tctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtgttttc 184
           : :  :   :  ::: :::::::   ::: :::::| :: :: :: :   :: |:::|:
Db     852 KRDTADWKAWAAWRWRWRRDRKDRRGRRDRWRRWRGADKKWKWDDDDTAKDDWTKKDTDW 911

Qy     185 tgaataacatttgtgtggtgggttctttggaaggagtgag 224
           |  |||  :::: :: : ::| :: |::: : |  ::|::
Db     912 TAGATAGWDDDKAKDGDWKRGTDWRTWKRTWKGWGRKGDK 951


RESULT  11
CNS00Z7O
LOCUS       CNS00Z7O               1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN01O10 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL097326
VERSION     AL097326.1  GI:5608937
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
  MMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN01O10"
                     /note="end : SP6"
BASE COUNT      258 a    185 c    199 g    324 t    135 others
ORIGIN


  Query Match             14.9%;  Score 35.6;  DB 12;  Length 1101;
  Best Local Similarity   34.4%;  Pred. No. 15;
  Matches   62;  Conservative   39;  Mismatches   79;  Indels    0;  Gaps    0;

Qy      60 gagtggatctccaaggaccaggttatttttaaaaaagatttgttttgtcaagtgtcatatgt 119
           || || :   : ::|||:  |::| |:|| :::   ||| |||: :| |      | | |
Db     885 GAATGTMAWMMAMMGGAMTGGSYTTTKTTTWDVTCCTTTTTTTYTWCGATMAGTYTTTTT 944

Qy     120 aggtgtctgcacccaggggtggggaatgtttgggcagaagggagaaggatctagaatgtg 179
             | ||: : | | ||||:|||   | | | :     : : |  ||   : |  | ||
Db     945 TTTTTTCYTBKCTCGGGGGKGGGGGGGGGTGGWRGGTTTKTKTGKGGGKGGKGGGBTTTG 1004

Qy     180 ttttctgaataacatttgtgtggtgggttctttggaaggagtgagatcattttcttatct 239
           ||||:| : :     : ::| :: :  || :||::  :: |:: : :   :  ||| | |
Db    1005 TTTTBTTMKDTGKKGKGKKGGKKGBACTTTKTTKKGKKKGGKKKKGKGGGKCCCTTTTTT 1064


RESULT  12
AQ260214/c
LOCUS       AQ260214               376 bp    DNA     linear   GSS 24-OCT-1998
DEFINITION  CITBI-E1-2515D9.TR CITBI-E1 Homo sapiens genomic clone 2515D9, DNA
            sequence.
ACCESSION   AQ260214
VERSION     AQ260214.1  GI:3786738
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of a random human BAC End Sequence Database for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1998)
COMMENT     Other GSSs: CITBI-E1-2515D9.TF
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2515D9"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT      145 a     55 c     51 g    125 t
ORIGIN


  Query Match             14.8%;  Score 35.4;  DB 12;  Length 376;
  Best Local Similarity   50.9%;  Pred. No. 14;
  Matches   84;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;

Qy      39 tgtttgcaatggtgttgccctgagtggatctccaaggaccaggttattttaaaaagattt 98
           |||||  ||   | |    || |||||| |  | | |  || | |  ||||| | || || |
Db     310 TGTTTTGAAAACTATAAAGCTAAGTGGAGCCACGATCACAAAGCAATTTTCAGAATATAT 251

Qy      99 gttttgtcaagtgtcatatgtaggtgtctgcacccaggggtggggaatgtttgggcagaa 158
           | |  | | ||  |  ||| || || | || |  ||  | |     |||| ||   |||
Db     250 ATGTAATTACGTATATTATCTATGTATTTGTAGACATAGTTTTCTTATGTGTGATGAGAG 191

Qy     159 gggagaaggatctagaatgtgttttctgaataacatttgtgtggt 203
               |  | |  ||  |||  |    |||   |   |||| |
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Db    190 AACTACAACTTTTGAAAAATGTGATAGTTATACTTTGCCTGTGAT 146


RESULT  13
AZ589172
LOCUS       AZ589172                637 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0398A06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0398A06 F, DNA sequence.
ACCESSION   AZ589172
VERSION     AZ589172.1  GI:11711362
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0398  row: A  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 637.
FEATURES             Location/Qualifiers
     source          1. .637
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0398A06"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      157 a    154 c    151 g    175 t
ORIGIN


  Query Match             14.8%;  Score 35.4;  DB 12;  Length 637;
  Best Local Similarity   54.1%;  Pred. No. 15;
  Matches   72;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy      24 gatgttacatcacagtgtttgcaatggtgttgccctgagtggatctccaaggaccaggtt 83
```

```
Db    436 GAAATTGGAGCAGTGTGGTAGCATTGTCCCTGTCCCCATTGGAACTTGAAGAAATTAAAA 495

Qy     84 attttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtgggg 143
          | ||||||||  ||  |||     | |  | |||    |||| || || || | ||| |
Db    496 CTGTTAAAAATTTTGTTTTACATTATTTGCTTATTACTGTGTGTGAACACATGTGTGTGC 555

Qy    144 aatgtttgggcag 156
          |||  ||   ||
Db    556 TATGCATGCAAAG 568


RESULT  14
CNS015FK/c
LOCUS       CNS015FK                897 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN13G14 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL105386
VERSION     AL105386.1  GI:5617400
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 897)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .897
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN13G14"
                     /note="end : SP6"
BASE COUNT      227 a    67 c    112 g    175 t    316 others
ORIGIN


  Query Match             14.7%;  Score 35.2;  DB 12;  Length 897;
  Best Local Similarity   29.4%;  Pred. No. 19;
  Matches   63;  Conservative   56;  Mismatches   95;  Indels    0;  Gaps    0;

Qy     24 gatgttacatcacagtgtttgcaatggtgttgccctgagtggatctccaaggaccaggtt 83
          | : ||: :|   : : |:    :| :  |::   |:::::: : :  |  :   |:
Db    894 GTWTTTRWDTKTTRWWTTWAATKWTARAATWRTATTDWKWRRTWWWTGAGTRTAKAKAAA 835

Qy     84 attttaaaaagatttgttttgtcaagtgtcatatgtaggtgtctgcacccaggggtgggg 143
          | :::: |  | ||| ||:|    : :   || : ||    : || |   :|    :|:|
Db    834 ARWKDDGGGATTTTTTTTWTWAWTWAWTAWATTWWTATTAAWKTGAAAGAMGCTTGDGKG 775

Qy    144 aatgtttgggcagaagggagaaggatctagaatgtgttttctgaataacatttgtgtggt 203
            |:|||:::  |: :: : ||  ||  :  :::: ::|| |  |||   | |:| ||
Db    774 TKTKTTTKKBTTGMGKVTWAAATAATTAWTTWKDWTDWTTKTATATATTYTATDTATGAA 715

Qy    204 gggttctttggaaggagtgagatcattttcttat 237
           ::|| |||  ||: : |:| || ::  | :|||
Db    714 TKVTTTTTTATAARARTTKATATARWAATTKTAT 681
```

```
RESULT  15
CNS004YY/c
LOCUS       CNS004YY                859 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR11F03 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL055406
VERSION     AL055406.1  GI:4932207
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE.  1  (bases 1 to 859)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
   'MENT    Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES .              Location/Qualifiers
     source             1. .859
                        /organism="Drosophila melanogaster"
                        /db_xref="taxon:7227"
                        /clone_lib="RPCI-98"
                        /clone="BACR11F03"
                        /note="end : TET3"
BASE COUNT      302 a     32 c     15 g    124 t    386 others
ORIGIN


  Query Match           14.6%;  Score 34.8;  DB 12;  Length 859;
  Best Local Similarity   13.9%;  Pred. No. 24;
  Matches   25;  Conservative   91;  Mismatches   64;  Indels    0;  Gaps    0;

Qy      46 aatggtgttgccctgagtggatctccaaggaccaggttatttttaaaaagatttgtttttgt 105
           ::|::|:| :   |::: :::     :::::  :::| :|||||:::: ::: |::|  :
Db     816 RRTDRTRTRRRRRTRRRRRRRRRRRRRRRRRTRRRRTRRTTTTRRRRTRRWRTRDTRARR 757

Qy     106 caagtgtcatatgtaggtgtctgcacccaggggtggggaatgtttgggcagaagggagaa 165
            :::  |  |  : :::|:| :  :   : : : :::: : : |:::   ::::::::::
Db     756 WRRRRTTTTTTRDRRRRTRTTDTRDTDTRTRTRRRRDRTRRRRTDRRTRTRDRRRRRDRR 697

Qy     166 ggatctagaatgtgttttctgaataacatttgtgtggtgggttctttggaaggagtgaga 225
           ::::  :::: :   |    :|: :: ::||  |:::|  :|  |     :|:::: ::::
Db     696 DRDWDRDRRRRRGTRTRRRRDARRRRRRDTTTRGDRRTTTDTRRTARTTRARRRRGRRKR 637


Search completed: June 13, 2002, 15:17:37
Job time: 8874 sec
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